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## RESULT 12

ARL18507  
LOCUS ARL18507 5712 bp DNA linear PAT 16-MAY-2001  
DEFINITION Sequence 1 from patent US 6149903.  
ACCESSION ARL18507  
VERSION ARL18507.1 GI:14100417  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 5712)  
AUTHORS Holt,J.T., Jensen,R.A., King,M.-C., Page,D.L., Szabo,C.I.,  
Jettan,T.L., Robinson-Benion,C.L. and Thompson,M.E.  
TITLE Characterized BRCA1 and BRCA2 proteins and screening and  
therapeutic methods based on characterized BRCA1 and BRCA2 proteins  
JOURNAL Patent: US 6149903-A 1 21-NOV-2000;  
FEATURES  
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## ORIGIN

Query Match 99.8%; Score 5701.4; DB 6; Length 5712;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 5705; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
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RESULT 13  
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DEFINITION Sequence 1 from patent US 6177410.  
ACCESSION ARI25601  
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KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
AUTHORS 1 (bases 1 to 5712)  
Holt, J. T., Jensen, R. A., King, M. -C., Steiner, M. S.,  
Robinson-Berlin, C. L. and Thompson, M. E.  
TITLE Therapeutic methods for prostate cancer  
JOURNAL Patent: US 6177410-A 1 23-JAN-2001;  
FEATURES Location/Qualifiers  
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ORIGIN  
Query Match 99.8%; Score 5701.4; DB 6; Length 5712;  
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## RESULT 14

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Sequence 47 from patent US 6342483.

AR184044  
ACCESSION

AR184044.1 GI:20228013

## KEYWORDS

Unknown.

ORGANISM

Unclassified.

1 (bases 1 to 5712)

REFERENCE  
Holt, J.T., Jensen, R.A., Page, D.L., Obermiller, P.S.,  
Robinson-Bennett, C.L. and Thompson, M.E.

TITLE  
Method for detection and treatment of breast cancer

JOURNAL  
Patent: US 6342483-A 47 29-JAN-2002;

FEATURES  
Location/Qualifiers

1..5712  
source

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RESULT 15
LOCUS   AR004673
DEFINITION Sequence 1 from patent US 5747282.
ACCESSION AR004673
VERSION AR004673.1 GI:3965552
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
AUTHORS Skolnick,M.H., Goldgar,D.B., Miki,Y., Swenson,J., Kamb,A.,
Harsman,K.D., Shattuck-Eidens,D.M., Tavtigian,S.V., Wiseman,R.W.
and Futreal,P.Andrew.
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JOURNAL Patent: US 5747282-A 1 05-MAY-1998;
FEATURES
source 1. .5914
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ORIGIN
Query Match 99.8%; Score 5701.4; DB 6; Length 5914;
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Matches 5705; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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Db      361  AACTGTGTGAAGAGCTTATTGAAAATCATTGTGTCTTTTTCAGCTTGACACAGGTTGGAGT 420
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5401 TCAGGGGGCTAGAAATCTGTTGCTATGGGCCCTTCAACCAATGCCCACAGATCAACTGG 5460  
5401 TCAGGGGGCTAGAAATCTGTTGCTATGGGCCCTTCAACCAATGCCCACAGATCAACTGG 5460  
5461 AATGGATGCTAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5520  
5461 AATGGATGCTAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5520  
5521 GCACAGGTGTCCAACCAATTTGTTGCTGAGCAGCAGATGCTGAGCAGAGGACAAATGGCT 5580  
5521 GCACAGGTGTCCAACCAATTTGTTGCTGAGCAGCAGATGCTGAGCAGAGGACAAATGGCT 5580  
5581 TCCATGCAATTTGGGAGATGCTGAGGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5640  
5581 TCCATGCAATTTGGGAGATGCTGAGGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5640  
5641 GTGTAGCACTTACCAAGTCCAGAGGAGCTGGAACCTTACCTGATACCCAGATGCTGCTGCTG 5700  
5641 GTGTAGCACTTACCAAGTCCAGAGGAGCTGGAACCTTACCTGATACCCAGATGCTGCTGCTG 5700  
5701 GCCACTACTGGA 5711  
5701 GCCACTACTGGA 5711

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Mon Jun 14 09:16:01 2004

Search completed: June 12, 2004, 02:48:07  
Job time : 21408 secs



CC or may not have an increased susceptibility to breast or ovarian cancer.  
CC The sequences used identify gene changes which are due to polymorphisms,  
CC rather than cancer causing mutations. BRCA1 is an anti-oncogene (tumour  
CC suppressor) which is involved in genetic inheritance of cancers,  
CC especially breast and ovarian cancer. It is found at human chromosome 17q  
CC which is known to be linked to cancer susceptibility, especially breast  
CC cancer. Cells containing a mutation in this gene lose the wild-type  
CC function of BRCA1 and are more susceptible to cancers  
XX  
SQ Sequence 5711 BP; 1953 A; 1098 C; 1277 G; 1393 T; 0 U; 0 Other;  
Query Match 100.0%; Score 5589; DB 2; Length 5711;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 5589; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ATGGGATTTATCTGCTCTTCGCGTGTGAAGAGTACAAATGTCTAATATGCTATGCAGAAA 60  
DB 120 ATGGATTTATCTGCTCTTCGCGTGTGAAGAGTACAAATGTCTAATATGCTATGCAGAAA 179  
QY 61 ATCTTAGAGTGTCCCATCTGCTGCGATGATCAAGGAACCTGTCTCCCAAAAGTGTGAC 120  
DB 180 ATCTTAGAGTGTCCCATCTGCTGCGATGATCAAGGAACCTGTCTCCCAAAAGTGTGAC 239  
QY 121 CACATATTTTGCATATTTTGCATGCTGAACTTCTCAACCAAGAAAGGGCTTTCACAG 180  
DB 240 CACATATTTTGCATATTTTGCATGCTGAACTTCTCAACCAAGAAAGGGCTTTCACAG 299  
QY 181 TGTCTTTATGTAAGATGATATAACCAAAAGGAGCTTCAAGAAAGTACGAGATTTAGT 240  
DB 300 TGTCTTTATGTAAGATGATATAACCAAAAGGAGCTTCAAGAAAGTACGAGATTTAGT 359  
QY 241 CAATCTGTGAGAGCTATGAAATCATTTGCTGCTTTTTCAGCTTGAACAGGTTTGGAG 300  
DB 360 CAATCTGTGAGAGCTATGAAATCATTTGCTGCTTTTTCAGCTTGAACAGGTTTGGAG 419  
QY 301 TATGCAAAACAGCTATATTTTGCATATTTTGCATATTTTGCATATTTTGCATATTTTGCAT 360  
DB 420 TATGCAAAACAGCTATATTTTGCATATTTTGCATATTTTGCATATTTTGCATATTTTGCAT 479  
QY 361 GAAGTTTCTATCATCAAGTATGGCTACAGAAACCGTGCAGAAAGCTTCTACAGAGT 420  
DB 480 GAAGTTTCTATCATCAAGTATGGCTACAGAAACCGTGCAGAAAGCTTCTACAGAGT 539  
QY 421 GAACCCGAAATCTCTCTGCGAGAAACCAAGTCTCAGTGTCCAACTCTCTAACTCTGGA 480  
DB 540 GAACCCGAAATCTCTCTGCGAGAAACCAAGTCTCAGTGTCCAACTCTCTAACTCTGGA 599  
QY 481 ACTGTGAGAACTCTGAGGCAAGCAGCGGATACAACTCTCAAGAGACGCTGTCTACATT 540  
DB 600 ACTGTGAGAACTCTGAGGCAAGCAGCGGATACAACTCTCAAGAGACGCTGTCTACATT 659  
QY 541 GAATTTGGGATCTGATTTCTTCAAGATACCGTTTAAAGGCAACTTATGCGAGTGTGGA 600  
DB 660 GAATTTGGGATCTGATTTCTTCAAGATACCGTTTAAAGGCAACTTATGCGAGTGTGGA 719  
QY 601 GATCAAGAAATGTTTCAAAATCAACCTCTCAAGGAACCGGATGAAATCAGTTTGGATTTCT 660  
DB 720 GATCAAGAAATGTTTCAAAATCAACCTCTCAAGGAACCGGATGAAATCAGTTTGGATTTCT 779  
QY 661 GCAAAAAAGGCTGTGTGTGAATTTTCTGAGAGCGGATGAAATACATGACATCATCAA 720  
DB 780 GCAAAAAAGGCTGTGTGTGAATTTTCTGAGAGCGGATGAAATACATGACATCATCAA 839  
QY 721 CCCAGTAATATGATTTGAAACCACTGAGAGCGGATGAGGATCCAGAGAAAG 780  
DB 840 CCCAGTAATATGATTTGAAACCACTGAGAGCGGATGAGGATCCAGAGAAAG 899  
QY 781 TATCAGGAGTGTCTGTTTCAAACTTGTGAGGCGATGTGGGCAAAATCTCATGCC 840  
DB 900 TATCAGGAGTGTCTGTTTCAAACTTGTGAGGCGATGTGGGCAAAATCTCATGCC 959  
QY 841 AGCTCATTTACAGCATGAGAAACAGCAGTTTATTTACTTCACTAAAGACAGAAATCAATGTAGAA 900

DB 960 AGCTCATTTACAGCATGAGAAACAGCAGTTTATTTACTCACTAAAGACAGAAATCAATGTAGAA 1019  
QY 901 AAGCTGAAATCTGTATTAATAAGCAAAACAGCCTTGCTTAGCAAGAGCCCAATAACAGA 960  
DB 1020 AAGCTGAAATCTGTATTAATAAGCAAAACAGCCTTGCTTAGCAAGAGCCCAATAACAGA 1079  
QY 961 TGGGCTGGAAGTAAAGGAAACATGTAATGATAGGCGGACTCCCGACACAGAAAAAAGGTA 1020  
DB 1080 TGGGCTGGAAGTAAAGGAAACATGTAATGATAGGCGGACTCCCGACACAGAAAAAAGGTA 1139  
QY 1021 GATCTGAATCTGATCCCTGTGTGAGAGAAAAAGATGGAATAGAGAAACTGCCATGC 1080  
DB 1140 GATCTGAATCTGATCCCTGTGTGAGAGAAAAAGATGGAATAGAGAAACTGCCATGC 1199  
QY 1081 TCAGAGAACTCTAGAGATCTGAAAGATGTTCTTTGGATTAACACTAAATAGCAGCATTTGAG 1140  
DB 1200 TCAGAGAACTCTAGAGATCTGAAAGATGTTCTTTGGATTAACACTAAATAGCAGCATTTGAG 1259  
QY 1141 AAGCTTAATGATGTGTTTTTCCAGAAAGTGAACCTGTTAGTCTGATGACTCATCATGAT 1200  
DB 1260 AAGCTTAATGATGTGTTTTTCCAGAAAGTGAACCTGTTAGTCTGATGACTCATCATGAT 1319  
QY 1201 GGGGAGTCTGAATCAAAATGCCAAAGTAGCTGATGTTTGGACGTTCTTAAATGAGCTAGAT 1260  
DB 1320 GGGGAGTCTGAATCAAAATGCCAAAGTAGCTGATGTTTGGACGTTCTTAAATGAGCTAGAT 1379  
QY 1261 GAATATTTCTGTTCTTCCAGAGAAAAATAGACTTACTGCGCAGTGAATCTCTCATGAGCTTTA 1320  
DB 1380 GAATATTTCTGTTCTTCCAGAGAAAAATAGACTTACTGCGCAGTGAATCTCTCATGAGCTTTA 1439  
QY 1321 ATATGTAAGAGTGAAGAGTTCTACTCCAAATCAGTGAAGAGTATATTTGAGACAAATA 1380  
DB 1440 ATATGTAAGAGTGAAGAGTTCTACTCCAAATCAGTGAAGAGTATATTTGAGACAAATA 1499  
QY 1381 TTTGGGAAAACTTATCGGAAGAAAGCGCTCCCAACTTTAAGCCATGTAACCTGAAAAAT 1440  
DB 1500 TTTGGGAAAACTTATCGGAAGAAAGCGCTCCCAACTTTAAGCCATGTAACCTGAAAAAT 1559  
QY 1441 CTAAATTTAGAGCATTTGTTTCTGAGCCACAGATATTAAGAGGCTCCCTCACAAT 1500  
DB 1560 CTAAATTTAGAGCATTTGTTTCTGAGCCACAGATATTAAGAGGCTCCCTCACAAT 1619  
QY 1501 AAATTTAAGCGTAAAGAGAGACCTTACATCAGGCTTCTCATCTGAGGATTTTATCAAGAA 1560  
DB 1620 AAATTTAAGCGTAAAGAGAGACCTTACATCAGGCTTCTCATCTGAGGATTTTATCAAGAA 1679  
QY 1561 GCAGATTTGGCAGTTTCAAAAGACTCTCTGAAATGATATAATCAGGGAACCTAACCAACCGAG 1620  
DB 1680 GCAGATTTGGCAGTTTCAAAAGACTCTCTGAAATGATATAATCAGGGAACCTAACCAACCGAG 1739  
QY 1621 CAGAACTGCTCAAGTGTGATTAATTTACTAATAGTGTCTCATCAGAAATAAAACAAAAGGTGAT 1680  
DB 1740 CAGAACTGCTCAAGTGTGATTAATTTACTAATAGTGTCTCATCAGAAATAAAACAAAAGGTGAT 1799  
QY 1681 TCTATTGAGAAATGAGAAAAATCTCTAAACCAATAGATTCATCTCGAAAAAGAAATCTGCTTTC 1740  
DB 1800 TCTATTGAGAAATGAGAAAAATCTCTAAACCAATAGATTCATCTCGAAAAAGAAATCTGCTTTC 1859  
QY 1741 ARAACGAAAGCTGAACCTATAAGCAGCAGTATTAAGCAATATGGAATCTGAAATTAATATTC 1800  
DB 1860 ARAACGAAAGCTGAACCTATAAGCAGCAGTATTAAGCAATATGGAATCTGAAATTAATATTC 1919  
QY 1801 CACAATTTCAAAAGCACTTAAAAAGATAGCTCAGGAGGAGTCTTCTTACAGGCAATATT 1860  
DB 1920 CACAATTTCAAAAGCACTTAAAAAGATAGCTCAGGAGGAGTCTTCTTACAGGCAATATT 1979  
QY 1861 CATGCGCTTGAATCTAGTGTGAGTGAATCTTAAGCCCACTTAATTTGATCTGAAATTTGCAA 1920  
DB 1980 CATGCGCTTGAATCTAGTGTGAGTGAATCTTAAGCCCACTTAATTTGATCTGAAATTTGCAA 2039  
QY 1921 ATTGATAGTGTGTTCTAGCAGTGAAGAGATAAAGAAAAAGATGACCAACCAATGCCAGTGC 1980  
DB 2040 ATTGATAGTGTGTTCTAGCAGTGAAGAGATAAAGAAAAAGATGACCAACCAATGCCAGTGC 2099



1981 AGGCCAGCAGAAACCTCAACTCATGGAAGGTAAAGAACCTGCAACTGAGCCCAAGAG 2040  
Db AGGCCAGCAGAAACCTCAACTCATGGAAGGTAAAGAACCTGCAACTGAGCCCAAGAG 2159  
1982 AGTACAGCCCAATCAAGCAGCAAGTAAAGACATGACAGTGTATCTTCCAGAGCTG 2100  
Db AGTACAGCCCAATCAAGCAGCAAGTAAAGACATGACAGTGTATCTTCCAGAGCTG 2219  
1983 AAGTTAAACAAATGCACTGCTTCTTTTACTAGTGTCAAAATACCAAGTGAATCAAGAA 2279  
Qy AAGTTAAACAAATGCACTGCTTCTTTTACTAGTGTCAAAATACCAAGTGAATCAAGAA 2160  
Db AAGTTAAACAAATGCACTGCTTCTTTTACTAGTGTCAAAATACCAAGTGAATCAAGAA 2220  
1984 TTGTCAATCTAGCTTCCAGAGCAAGAAAGAGCAAGTAAAGTGAATCAAGTGAATG 2280  
Qy TTGTCAATCTAGCTTCCAGAGCAAGAAAGAGCAAGTAAAGTGAATCAAGTGAATG 2339  
Db TTGTCAATCTAGCTTCCAGAGCAAGAAAGAGCAAGTAAAGTGAATCAAGTGAATG 2280  
1985 TCTAATAATGCTGAAGCAAGCCCAAGATCTCATGTTAAGTGAAGAGGTTTGCACACT 2399  
Qy TCTAATAATGCTGAAGCAAGCCCAAGATCTCATGTTAAGTGAAGAGGTTTGCACACT 2340  
Db TCTAATAATGCTGAAGCAAGCCCAAGATCTCATGTTAAGTGAAGAGGTTTGCACACT 2459  
1986 GAAAGATCTGTAGAGATGACAGTATTTCACTGGTACCTGGTATCTAATTGSCACTCAG 2400  
Qy GAAAGATCTGTAGAGATGACAGTATTTCACTGGTACCTGGTATCTAATTGSCACTCAG 2460  
Db GAAAGATCTGTAGAGATGACAGTATTTCACTGGTACCTGGTATCTAATTGSCACTCAG 2579  
1987 GAAAGTATCTGTTACTGCAAGTGTAGCACTCTAGGCAAGGCAAAACAGAAACCAATAAA 2580  
Qy GAAAGTATCTGTTACTGCAAGTGTAGCACTCTAGGCAAGGCAAAACAGAAACCAATAAA 2640  
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1988 TGTGTGAGTCAAGTGTGCAAGTGTGAAACCCCAAGGCACTAATTCACTGGTGTTCCAA 2699  
Qy TGTGTGAGTCAAGTGTGCAAGTGTGAAACCCCAAGGCACTAATTCACTGGTGTTCCAA 2640  
Db TGTGTGAGTCAAGTGTGCAAGTGTGAAACCCCAAGGCACTAATTCACTGGTGTTCCAA 2639  
1989 GATAATAGAAATGACACAGAGCTTTAAGTATCCATGGGACGTAAGTAAACACAGT 2580  
Qy GATAATAGAAATGACACAGAGCTTTAAGTATCCATGGGACGTAAGTAAACACAGT 2640  
Db GATAATAGAAATGACACAGAGCTTTAAGTATCCATGGGACGTAAGTAAACACAGT 2699  
1990 CGGGAACCAAGCATAGAAATGGAAGAAAGTGAACCTTGATGCTCAGTATTTGCAAGATA 2700  
Qy CGGGAACCAAGCATAGAAATGGAAGAAAGTGAACCTTGATGCTCAGTATTTGCAAGATA 2819  
Db CGGGAACCAAGCATAGAAATGGAAGAAAGTGAACCTTGATGCTCAGTATTTGCAAGATA 2760  
1991 TTCAAGGTTTCAAGGCGCAGTCAATTTGCTGTTTCAATCCAGGAAATGCAAGAG 2759  
Qy TTCAAGGTTTCAAGGCGCAGTCAATTTGCTGTTTCAATCCAGGAAATGCAAGAG 2820  
Db TTCAAGGTTTCAAGGCGCAGTCAATTTGCTGTTTCAATCCAGGAAATGCAAGAG 2939  
1992 GAATGTGCAACATTTCTGCGCCACTCTGGGTCTTAAAGAAACCAAGTCCAAAGTCACT 2700  
Qy GAATGTGCAACATTTCTGCGCCACTCTGGGTCTTAAAGAAACCAAGTCCAAAGTCACT 2819  
Db GAATGTGCAACATTTCTGCGCCACTCTGGGTCTTAAAGAAACCAAGTCCAAAGTCACT 2760  
1993 TTGAAATGTGAACAAAGGAAGAAATCAAGGAAAGATGAGTCTAATATCAAGCCTGTA 2879  
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Db TTGAAATGTGAACAAAGGAAGAAATCAAGGAAAGATGAGTCTAATATCAAGCCTGTA 2939  
1994 CAGACAGTTAAATCACTGAGGCTTTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 2880  
Qy CAGACAGTTAAATCACTGAGGCTTTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 2940  
Db CAGACAGTTAAATCACTGAGGCTTTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 3059  
1995 AATGCCAAATGTAGTATCAAGAGGCTCTAGGTTTGTCTATCATCTCAGTTCAGAGGC 2880  
Qy AATGCCAAATGTAGTATCAAGAGGCTCTAGGTTTGTCTATCATCTCAGTTCAGAGGC 2940  
Db AATGCCAAATGTAGTATCAAGAGGCTCTAGGTTTGTCTATCATCTCAGTTCAGAGGC 3059  
1996 AAGGAACTGGACTCAATTAATCAATTAATCAATTAATCAATTAATCAATTAATCAATTA 2940  
Qy AAGGAACTGGACTCAATTAATCAATTAATCAATTAATCAATTAATCAATTAATCAATTA 3000  
Db AAGGAACTGGACTCAATTAATCAATTAATCAATTAATCAATTAATCAATTAATCAATTA 3119  
1997 CCACCACTTTTCCCACTCAAGTCAATTTGTTTAAACTTAAATGTAAAGAAATCTGCTAG 3000  
Qy CCACCACTTTTCCCACTCAAGTCAATTTGTTTAAACTTAAATGTAAAGAAATCTGCTAG 3060  
Db CCACCACTTTTCCCACTCAAGTCAATTTGTTTAAACTTAAATGTAAAGAAATCTGCTAG 3179  
1998 GAAACCTTTGAGGAAATTTCAATGTCACTGAAAGAGAAATGGGAAATGAGAAATTTCCA 3179  
Qy GAAACCTTTGAGGAAATTTCAATGTCACTGAAAGAGAAATGGGAAATGAGAAATTTCCA 3120  
Db GAAACCTTTGAGGAAATTTCAATGTCACTGAAAGAGAAATGGGAAATGAGAAATTTCCA 3179

3061 AGTACAGTGCACCAATTTAGCCGTATTAACATTTAGAGAAATGTTTTTAAAGGAGCCAGC 3120  
Db AGTACAGTGCACCAATTTAGCCGTATTAACATTTAGAGAAATGTTTTTAAAGGAGCCAGC 3239  
3121 TCAACGCAATATTAATGAAGTAGGTTCCAGTACTAATGAAGTGGGCTCCAGTATTAATGAA 3180  
Qy TCAACGCAATATTAATGAAGTAGGTTCCAGTACTAATGAAGTGGGCTCCAGTATTAATGAA 3299  
Db TCAACGCAATATTAATGAAGTAGGTTCCAGTACTAATGAAGTGGGCTCCAGTATTAATGAA 3240  
3181 ATAGGTTCCAGTATGAAGAAATTTCAAGCAGAACTAGTGTAGAAACAGAGGCGCAAAATG 3240  
Qy ATAGGTTCCAGTATGAAGAAATTTCAAGCAGAACTAGTGTAGAAACAGAGGCGCAAAATG 3359  
Db ATAGGTTCCAGTATGAAGAAATTTCAAGCAGAACTAGTGTAGAAACAGAGGCGCAAAATG 3300  
3241 AATGCTATGCTTAGATAGGCTTTGCAACCTGAGTCTATAAACAAGTCTTCTCTGGA 3419  
Qy AATGCTATGCTTAGATAGGCTTTGCAACCTGAGTCTATAAACAAGTCTTCTCTGGA 3360  
Db AATGCTATGCTTAGATAGGCTTTGCAACCTGAGTCTATAAACAAGTCTTCTCTGGA 3479  
3301 AGTAATGTAGCATCTGAAATATAAAGCAAGTAATGAAGAGTGTAGTTCAGACTGTT 3360  
Qy AGTAATGTAGCATCTGAAATATAAAGCAAGTAATGAAGAGTGTAGTTCAGACTGTT 3420  
Db AGTAATGTAGCATCTGAAATATAAAGCAAGTAATGAAGAGTGTAGTTCAGACTGTT 3539  
3361 AATACAGATTTCTCTCCATATCTGATTTTCAATTAAGTGTAGTGTAGTGTAGTGTAGT 3420  
Qy AATACAGATTTCTCTCCATATCTGATTTTCAATTAAGTGTAGTGTAGTGTAGTGTAGT 3599  
Db AATACAGATTTCTCTCCATATCTGATTTTCAATTAAGTGTAGTGTAGTGTAGTGTAGT 3480  
3421 CATGCATCTCAGGTTTGTCTGAGACACCTCATGACCTGTGTAGTGTAGTGTAGTGTAGT 3480  
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Db CATGCATCTCAGGTTTGTCTGAGACACCTCATGACCTGTGTAGTGTAGTGTAGTGTAGT 3540  
3481 GAGAGTATCTAGTTTGTGTAATGACATTAAGGAAAGTCTGCTGTTTGTAGTGTAGTGTAGT 3600  
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3661 GAAGAGCTTCTCCTGCTTCCACATCTGTTTATTTGTTAAAGTAAACAAATATACCTTCTCAG 3720  
Qy GAAGAGCTTCTCCTGCTTCCACATCTGTTTATTTGTTAAAGTAAACAAATATACCTTCTCAG 3839  
Db GAAGAGCTTCTCCTGCTTCCACATCTGTTTATTTGTTAAAGTAAACAAATATACCTTCTCAG 3780  
3721 TCTACTAGGCATAGCACCGTTGCTACCGAGTGTCTGTCTTAAGAACACAGAGAGAAATTTA 3780  
Qy TCTACTAGGCATAGCACCGTTGCTACCGAGTGTCTGTCTTAAGAACACAGAGAGAAATTTA 3899  
Db TCTACTAGGCATAGCACCGTTGCTACCGAGTGTCTGTCTTAAGAACACAGAGAGAAATTTA 3840  
3781 TTATCAATTTGAAGAAATAGCTTAAATGACCTGAGTAAACAGGTAATTTGGCAAGGCACTCT 3840  
Qy TTATCAATTTGAAGAAATAGCTTAAATGACCTGAGTAAACAGGTAATTTGGCAAGGCACTCT 3959  
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3841 CAGGAACATCACCTTTAGTGAGGAAACAAATATTTCTGCTAGCTGTTTCTTCTTCAAGTGC 3900  
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3901 AGTGAAATTTGAAGAACTGCACTGCAATTAACAACCCAGGATCTTCTTCTGATTTGTTCT 4079  
Qy AGTGAAATTTGAAGAACTGCACTGCAATTAACAACCCAGGATCTTCTTCTGATTTGTTCT 4020  
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3961 TCCAAACAAATGAGGCACTCAGTCTGAAAGCAGGAGTGTGCTGTAGTGAACAAGAAATG 4020  
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Db TCCAAACAAATGAGGCACTCAGTCTGAAAGCAGGAGTGTGCTGTAGTGAACAAGAAATG 4080  
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4081 ATGGAATTCAACTTAGGTTGAAGCAGTCTGAGTGTGAGTGTGAAGTGAAGTGTCTCTGAA 4140  
Qy ATGGAATTCAACTTAGGTTGAAGCAGTCTGAGTGTGAGTGTGAAGTGAAGTGTCTCTGAA 4259  
Db ATGGAATTCAACTTAGGTTGAAGCAGTCTGAGTGTGAGTGTGAAGTGAAGTGTCTCTGAA 4200  
4141 GACTGCTCAGGGCTATCTCTCAGAGTGAACATTTTAAACCACTCAGCAGAGGATACCATG 4200  
Qy GACTGCTCAGGGCTATCTCTCAGAGTGAACATTTTAAACCACTCAGCAGAGGATACCATG 4200

Db 4260 GACTGCTAGGGCTATCTCTCAGATGACATTTTAACCRCTCAGCAGAGGGATACCATTG 4319  
Qy 4201 CAACATAAAGCTGATGAAGCTCCAGCAGGAAATGGCTGAATAGAGCTGTGTAGAACAG 4260  
Db 4320 CAACATAAAGCTGATGAAGCTCCAGCAGGAAATGGCTGAATAGAGCTGTGTAGAACAG 4379  
Qy 4261 CATGGGAGCAGCCTTCTAAGCAGTACCCCTCCATCATTAAGTACCTCTTCGCCCTTGA 4320  
Db 4380 CATGGGAGCAGCCTTCTAAGCAGTACCCCTCCATCATTAAGTACCTCTTCGCCCTTGA 4439  
Qy 4321 GACCTGCGAAATCCAGAACCAAGCAGCATCAGAAAAAGCAGTATTAACTTTCAGAAAAAGT 4380  
Db 4440 GACCTGCGAAATCCAGAACCAAGCAGCATCAGAAAAAGCAGTATTAACTTTCAGAAAAAGT 4499  
Qy 4381 AGTGAATACCTTATAGCAGGAGTCCAGAGCCCTTCTGCTGCAAGAGTTTGAAGTGTCT 4440  
Db 4500 AGTGAATACCTTATAGCAGGAGTCCAGAGCCCTTCTGCTGCAAGAGTTTGAAGTGTCT 4559  
Qy 4441 GCAGATAGTCTTACCAAGTAAATTAAGAACCAAGCAGTGGAAAGGTCAATCCCTTCTAAA 4500  
Db 4560 GCAGATAGTCTTACCAAGTAAATTAAGAACCAAGCAGTGGAAAGGTCAATCCCTTCTAAA 4619  
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Db 4620 TGCCCATCATTAGATAGTGTGTACATGCACAGTGTCTCTGGAGTCTTTCAGAAATAGA 4679  
Qy 4561 AACTACCCATCTCAAGAGGAGTCAATTAAGGTGTGTATGTGGAGGACCAACAGCTGGAA 4620  
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Qy 4621 GAGTCTGGGCGACAGATTTGAGCGAAACATCTTAATTCGCAAGCAGAGATCTAGAGGGA 4680  
Db 4740 GAGTCTGGGCGACAGATTTGAGCGAAACATCTTAATTCGCAAGCAGAGATCTAGAGGGA 4799  
Qy 4681 ACCCTTACCTTGAATCTGATCAGCTCTCTCTGATGACCTGATCTGATCTGATCTCT 4740  
Db 4800 ACCCTTACCTTGAATCTGATCAGCTCTCTCTGATGACCTGATCTGATCTGATCTCT 4859  
Qy 4741 GAAAGCAGAGCCCGAGTCTGCTGTGTGTGGCAACATACCATCTTCAACCTCTGCAATG 4800  
Db 4860 GAAAGCAGAGCCCGAGTCTGCTGTGTGTGGCAACATACCATCTTCAACCTCTGCAATG 4919  
Qy 4801 AAGTCTCCCAATTTGAATTTGCAATCTCTCCAGGTCAGCTGCTGCTCACTACT 4860  
Db 4920 AAGTCTCCCAATTTGAATTTGCAATCTCTCCAGGTCAGCTGCTGCTCACTACT 4979  
Qy 4861 GATACTGCTGGTATAATGCAATGGAAGAAAGTGTGAGCAGGAGAGCCAGAAATTCACA 4920  
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Qy 5041 ACTGAAGAGTACTCATGTTGTTATGAAAACAGATGCTGAGTTTGTGTGAAACGACA 5100  
Db 5160 ACTGAAGAGTACTCATGTTGTTATGAAAACAGATGCTGAGTTTGTGTGAAACGACA 5219  
Qy 5101 CTGAATATTTTCTAGGAATTTGGGAGGAAATGGGTAGTACTTATTTCTGGGTGACC 5160  
Db 5220 CTGAATATTTTCTAGGAATTTGGGAGGAAATGGGTAGTACTTATTTCTGGGTGACC 5279  
Qy 5161 CAGTCTATTAAAGAAAGAAATGCTGAATGAGCATGATTTTGAAGTTCAGAGGAGATGTG 5220  
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Qy 5221 GTCAATGAGAACCAACCAAGTCTCAAGCGAGCAGAGAAATCCCGAGCAGAAATC 5280

Db 5340 GTCATGTGAAGAAACCAACCAAGGTCCAAAGCGACGAAGAAATCCCGAGCAGAAAGATC 5399  
Qy 5281 TTCAGGGGGCTAGAAAATCTGTTGCTATGGGCCCTTTCACCAACATGCCACAGATCAACTG 5340  
Db 5400 TTCAGGGGGCTAGAAAATCTGTTGCTATGGGCCCTTTCACCAACATGCCACAGATCAACTG 5459  
Qy 5341 GAATGGATGTGTACAGCTGTGTGTGTCTCTGTGTGAAGAGCTTTTCATCATTCACCCCTT 5400  
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Qy 5401 GGCAACAGTGTCCACCCAAATTTGTTGTTGTGAGCCAGATGCTTGGACAGAGGACAAATGGC 5460  
Db 5520 GGCAACAGTGTCCACCCAAATTTGTTGTTGTGAGCCAGATGCTTGGACAGAGGACAAATGGC 5579  
Qy 5461 TTCATGCAATTTGGGCGAGATGTGTGAGGCACTGTGTGTGACCCGAGAGTGGGTGTTGGAC 5520  
Db 5580 TTCATGCAATTTGGGCGAGATGTGTGAGGCACTGTGTGTGACCCGAGAGTGGGTGTTGGAC 5639  
Qy 5521 AGTGTAGCACTTACCAAGTGCAGAGGAGCTGAGAGCTGACCTGTGTGTGATACCCAGATCCCCCAG 5580  
Db 5640 AGTGTAGCACTTACCAAGTGCAGAGGAGCTGAGAGCTGACCTGTGTGTGATACCCAGATCCCCCAG 5699  
Qy 5581 AGCCACTAC 5589  
Db 5700 AGCCACTAC 5708  
RESULT 2  
AAC60794  
ID AAC60794 standard; cDNA; 5711 BP.  
XX AC AAC60794;  
XX AC  
XX 07-FEB-2001 (first entry)  
XX Human BRCA1 (omi2) nucleotide sequence SEQ ID NO:3.  
XX Human; BRCA1; chromosome 17; 17q21; breast cancer; ovarian cancer;  
XX gene therapy; diagnosis; cytostatic; genetic susceptibility; mutation;  
XX polymorphism; identification; ss.  
XX Homo sapiens.  
XX  
XX US6130322-A.  
XX PD 10-OCT-2000.  
XX 06-MAY-1998; 98US-00074476.  
XX PF  
XX 12-FEB-1996; 96US-00598591.  
XX PR 12-DEC-1997; 97US-00798691.  
XX PA (GENE-) GENE LOGIC INC.  
XX Zeng B, Thurber D, Olson SJ, Alvares CP, Allen ACP, Murphy PD;  
PI Critz BS;  
XX WPI; 2000-646756/62.  
XX P-PSDB; AAB24218.  
XX New coding sequence of the human BRCA1 gene, i.e. BRCA1 (omi2), useful in  
XX gene therapy, especially for preventing or treating breast or ovarian  
XX cancer, as well as for diagnosing or monitoring breast or ovarian cancer.  
XX Claim 1; Col 45-50; 56pp; English.  
XX AAC60793 to AAC60795 encode the human BRCA1 (omi1-3) proteins given in  
XX AAB24217 to AAB24219 respectively. BRCA1 is found on chromosome 17  
XX mapping to position 17q21. The BRCA1 (omi2) coding sequence is  
XX specifically claimed in the present invention. The BRCA1 (omi2) coding  
XX sequence is useful in gene therapy, especially for preventing or treating  
XX breast or ovarian cancer. It is also useful for diagnosing or monitoring  
XX breast or ovarian cancer. Furthermore, the BRCA1 (omi2) coding sequence



Qy	1921	ATTGATAGTTGTTCTTACGAGTGAAGAGATAAAGAAAAAAGATACAACTCCAGTC	1981
Db	2040	ATTGATAGTTGTTCTTACGAGTGAAGAGATAAAGAAAAAAGATACAACTCCAGTC	2099
Qy	1981	AGGCAAGAGAAAACTTACAACTCATGCAAGTGAAGAACTCTGCAACTGGAGCCAGAG	2040
Db	2100	AGGCAAGAGAAAACTTACAACTCATGCAAGTGAAGAACTCTGCAACTGGAGCCAGAG	2159
Qy	2041	AGTAAACAGCCAAATGAACAGACAAGTAAAGACATGACAGTGATCTTTCCAGAGCTG	2100
Db	2160	AGTAAACAGCCAAATGAAGACAAGTAAAGACATGACAGTGATCTTTCCAGAGCTG	2219
Qy	2101	AAGTTTAACAAAATGACACTGGTCTTTTACTAAGTGTTCATATATCCAGTGAACCTTAAAGAA	2160
Db	2220	AAGTTTAACAAAATGACACTGGTCTTTTACTAAGTGTTCATATATCCAGTGAACCTTAAAGAA	2279
Qy	2161	TTTGTCAATCTCTAGCTTTCCAGAGAGAAAAAGAGAACTAGAAAAAGTTTAAAGTG	2220
Db	2280	TTTGTCAATCTCTAGCTTTCCAGAGAGAAAAAGAGAACTAGAAAAAGTTTAAAGTG	2339
Qy	2221	TCTAATATATGCTGAAGACCCCAAGATCTCATGTTTAACTGGAGAAAGGGTTTTCACAACT	2280
Db	2340	TCTAATATATGCTGAAGACCCCAAGATCTCATGTTTAACTGGAGAAAGGGTTTTCACAACT	2399
Qy	2281	GAAAGATCTGTAGAGAGTAGCAGTATTTTCACTGGTACTCTGGTACTGATTAATGGCACTCAG	2340
Db	2400	GAAAGATCTGTAGAGAGTAGCAGTATTTTCACTGGTACTCTGGTACTGATTAATGGCACTCAG	2459
Qy	2341	GAAAGTATCTGGTTACTGGAAAGTTAGCACTCTAGGGAAGGCAAAAAAGAAACCAATATAA	2400
Db	2460	GAAAGTATCTGGTTACTGGAAAGTTAGCACTCTAGGGAAGGCAAAAAAGAAACCAATATAA	2519
Qy	2401	TGTGTGAGTCAAGTGTGACAGCATTTGAAAAACCCCAAGGACATAATTCATGTGTTGTCCAAA	2460
Db	2520	TGTGTGAGTCAAGTGTGACAGCATTTGAAAAACCCCAAGGACATAATTCATGTGTTGTCCAAA	2579
Qy	2461	GATATATAGAAATGACACAGAAAGGCTTTTAAGTATCCATTTGGGACATGAAGTTAAACCAAGT	2520
Db	2580	GATATATAGAAATGACACAGAAAGGCTTTTAAGTATCCATTTGGGACATGAAGTTAAACCAAGT	2639
Qy	2521	CGGGAACCAAGCATAGAAATGGAAGAAAGTGAACTTGATGCTCAGTATTTTGCAGATATACA	2580
Db	2640	CGGGAACCAAGCATAGAAATGGAAGAAAGTGAACTTGATGCTCAGTATTTTGCAGATATACA	2699
Qy	2581	TTCAAGGTTTCAAAGGCGAGTCAATTTGCTCTGTGTTTTCAAAATCCAGGAAATGCGAAGAG	2640
Db	2700	TTCAAGGTTTCAAAGGCGAGTCAATTTGCTCTGTGTTTTCAAAATCCAGGAAATGCGAAGAG	2759
Qy	2641	GAATGTGCAATTTCTCTGCCCTCTCGGCTCTTTAAGAAACAAAGTCCAAAGTCACT	2700
Db	2760	GAATGTGCAATTTCTCTGCCCTCTCTCGGCTCTTTAAGAAACAAAGTCCAAAGTCACT	2819
Qy	2701	TTTGAATGTGAACAAAAAGGAAGAAATCAAGGAAAGAAATGAGTCTAATATCAAGCTGTGA	2760
Db	2820	TTTGAATGTGAACAAAAAGGAAGAAATCAAGGAAAGAAATGAGTCTAATATCAAGCTGTGA	2879
Qy	2761	CAGACAGTTAATATACATGCGAGGCTTTCCTGTGGTTGGTCAGAAAGAAATAGCCAGTTGAT	2820
Db	2880	CAGACAGTTAATATACATGCGAGGCTTTCCTGTGGTTGGTCAGAAAGAAATAGCCAGTTGAT	2939
Qy	2821	AATGCCAAATGTAGTATCAAGGAGGCTCTAGGTTTTTGTCTATCTCTCAGTTCCAGAGC	2880
Db	2940	AATGCCAAATGTAGTATCAAGGAGGCTCTAGGTTTTTGTCTATCTCTCAGTTCCAGAGC	2999
Qy	2881	AACGAAACTGGAATCATTTACTCCAAATATAACATGGACTTTTACAAACCCATATTCGTATA	2940
Db	3000	AACGAAACTGGAATCATTTACTCCAAATATAACATGGACTTTTACAAACCCATATTCGTATA	3059
Qy	2941	CCAGCACTTTTCCCAATCAAGTCAATTTGTTTAAACTATAATGTAAGAAATCTGCTAGAG	3000
Db	3060	CCAGCACTTTTCCCAATCAAGTCAATTTGTTTAAACTATAATGTAAGAAATCTGCTAGAG	3119
Qy	3001	GAAAACTTTTGGGGAACATTCATATGTCACTCTGAAAGAGAAATGCGAAATGAGAACATTCACA	3060

Db	3120	GAAGAACTTTGAGGAACTTCAATGCTCACCTCATAGAGAAATGGAATGAGAACTTCCA	3179
Qy	3061	AGTACAGTGAGCACAATTTAGCCGTAATAACAATTAGAGAAATCTTTTAAAGAGCCAGC	3120
Db	3180	AGTACAGTGAGCACAATTTAGCCGTAATAACAATTAGAGAAATGTTTAAAGAGCCAGC	3239
Qy	3121	TCAAGCAATATAATATGAGTAGTGTCCAGTACTAATGAAGTGGCTCCAGTATTAATGAA	3180
Db	3240	TCAAGCAATATAATATGAGTAGTGTCCAGTACTAATGAAGTGGCTCCAGTATTAATGAA	3299
Qy	3181	ATAGGTTCCAGTGATGAATAACATTCAGCAGACTAGGTAGAACACAGAGGGCCAAATTTG	3240
Db	3300	ATAGGTTCCAGTGATGAATAACATTCAGCAGACTAGGTAGAACACAGAGGGCCAAATTTG	3359
Qy	3241	AATGCTATGCTTAGATTAGGGTTTTGCCAACCTGAGTCTATATAACAAAAGTCTTCCTGGA	3300
Db	3360	AATGCTATGCTTAGATTAGGGTTTTGCCAACCTGAGTCTATATAACAAAAGTCTTCCTGGA	3419
Qy	3301	AGTAATTTGTAAGCATCTCTGAAATAAATAAGCAAGAAATGAGAGAGTAGTTCAAGACTGTT	3360
Db	3420	AGTAATTTGTAAGCATCTCTGAAATAAATAAGCAAGAAATGAGAGAGTAGTTCAAGACTGTT	3479
Qy	3361	AATACAGATTCTCTCCATATCTGATTTAGATTAGAACTTAGAACAGCTATGGCAAGTAGT	3420
Db	3480	AATACAGATTCTCTCCATATCTGATTTAGAACTTAGAACAGCTATGGCAAGTAGT	3539
Qy	3421	CATGCATCTCAGGTTTTGTTCTGAGACACCTGATGACTGTTAGATGATGGTGAATAAAG	3480
Db	3540	CATGCATCTCAGGTTTTGTTCTGAGACACCTGATGACTGTTAGATGATGGTGAATAAAG	3599
Qy	3481	GAAGATATCTAGTTTTGCTGAAAAATGACATTAAGCAAGTTCTGCTGTTTTTACGAAAAAGC	3540
Db	3600	GAAGATATCTAGTTTTGCTGAAAAATGACATTAAGCAAGTTCTGCTGTTTTTACGAAAAAGC	3659
Qy	3541	GTCCAGAGAGGAGCTTAGCAGGAGTCTTAGCCCTTTTCCACCATACACATTGGCTCAG	3600
Db	3660	GTCCAGAGAGGAGCTTAGCAGGAGTCTTAGCCCTTTTCCACCATACACATTGGCTCAG	3719
Qy	3601	GGTTACCGAAGGGGCCAGAAATTAGAGTCTCTAGAGAGAACTTATCTAGTAGGAT	3660
Db	3720	GGTTACCGAAGGGGCCAGAAATTAGAGTCTCTAGAGAGAACTTATCTAGTAGGAT	3779
Qy	3661	GAAAGAGCTTCCCTGCTTCCAAACACTTGTTATTGTTAAAGTAAACAATACTCTCTCAG	3720
Db	3780	GAAAGAGCTTCCCTGCTTCCAAACACTTGTTATTGTTAAAGTAAACAATACTCTCTCAG	3839
Qy	3721	TCTACTAGGCATAGCACCGTTGCTACCGAGTGTCTCTTAAGAACACAGAGGAGAAATTTA	3780
Db	3840	TCTACTAGGCATAGCACCGTTGCTACCGAGTGTCTCTTAAGAACACAGAGGAGAAATTTA	3899
Qy	3781	TTATCATTTGAAGATAGCTTTAAATGATCGAGTAAACAGGTAAATATGGCAAGGCATCT	3840
Db	3900	TTATCATTTGAAGATAGCTTTAAATGATCGAGTAAACAGGTAAATATGGCAAGGCATCT	3959
Qy	3841	CAGGAAATCACTTATGAGGAGAAACAAATGTTCTGCTAGCTTGTGTTCTTCCAGTGC	3900
Db	3960	CAGGAAATCACTTATGAGGAGAAACAAATGTTCTGCTAGCTTGTGTTCTTCCAGTGC	4019
Qy	3901	AGTGAATTTGAAGCTTGATCGAAATAAACAACCCAGGATCCCTTCTTGATTCGTTCT	3960
Db	4020	AGTGAATTTGAAGCTTGATCGAAATAAACAACCCAGGATCCCTTCTTGATTCGTTCT	4079
Qy	3961	TCCAAACAAATGAGGCATCAGTCTGAAAGCCAGGGAGTTGGTCTCAGTGACAAGGAAATG	4020
Db	4080	TCCAAACAAATGAGGCATCAGTCTGAAAGCCAGGGAGTTGGTCTCAGTGACAAGGAAATG	4139
Qy	4021	GTGTTGATGATGAAGAGAGGACGGCTTTGAGAGAAAAATATCAGAGAGAGCAAGC	4080
Db	4140	GTGTTGATGATGAAGAGAGGACGGCTTTGAGAGAAAAATATCAGAGAGAGCAAGC	4199
Qy	4081	ATGGATTCAAACTTAGTCAAGCAGCATCTCGGTGTGAGAGTGAACCAAGGCTCTCTCAA	4140

Db 4200 ATGGATTCAAACTTAGGTGAAGCAGCATCTGGTGTGAGAGTCAAAACAGCGCTCTCTGAA 4259  
QY 4141 GACTGCTCAGGCGTATCCCTCTCAGAGTGACATTTTAAACCACTCAGCAGAGGAGATACCAATG 4200  
Db 4260 GACTGCTCAGGCGTATCCCTCTCAGAGTGACATTTTAAACCACTCAGCAGAGGAGATACCAATG 4319  
QY 4201 CAACATACTGATTAAGCTCCAGCAGGAATGGCTGAACCTAGAGAGCTGTGTGAACAG 4260  
Db 4320 CAACATACTGATTAAGCTCCAGCAGGAATGGCTGAACCTAGAGAGCTGTGTGAACAG 4379  
QY 4261 CATGGAGCCAGCTCTTAAACAGCTACCCCTCCATCATCAAGTGACCTCTTCTGCCCTTGAG 4320  
Db 4380 CATGGAGCCAGCTCTTAAACAGCTACCCCTCCATCATCAAGTGACCTCTTCTGCCCTTGAG 4439  
QY 4321 GACCTGCGAATTCAGAAACAAAGCAGCATCAGAAAAGCAATTAACCTTCACAGAAAGT 4380  
Db 4440 GACCTGCGAATTCAGAAACAAAGCAGCATCAGAAAAGCAATTAACCTTCACAGAAAGT 4499  
QY 4381 AGTGAATACCCCTATTAAGCCAGAAATCCAGAGGCCCTTCTGCTGACAGTTCAGAGTGCT 4440  
Db 4500 AGTGAATACCCCTATTAAGCCAGAAATCCAGAGGCCCTTCTGCTGACAGTTCAGAGTGCT 4559  
QY 4441 GCAGATAGTTCTACAGTAATAAATAAGAACCCAGAGTGGAAAGTCAATCCCTCTTAAA 4500  
Db 4560 GCAGATAGTTCTACAGTAATAAATAAGAACCCAGAGTGGAAAGTCAATCCCTCTTAAA 4619  
QY 4501 TGCCCATCATTAAGTAGATAGTGGTACATGACAGCTTCTGCTGACAGTTCAGAAATAGA 4560  
Db 4620 TGCCCATCATTAAGTAGATAGTGGTACATGACAGCTTCTGCTGACAGTTCAGAAATAGA 4679  
QY 4561 AACTACCATCTCAAGAGGAGCTCAATTAAGTGTGTGATGGAGGAGCAACAGCTGGAA 4620  
Db 4680 AACTACCATCTCAAGAGGAGCTCAATTAAGTGTGTGATGGAGGAGCAACAGCTGGAA 4739  
QY 4621 GAGTCGGGCGCACAGATTTGACGGAAACATCTTACTTGGCCAGGAGATCTAGAGGGA 4680  
Db 4740 GAGTCGGGCGCACAGATTTGACGGAAACATCTTACTTGGCCAGGAGATCTAGAGGGA 4799  
QY 4681 ACCCTTACCTGGATCTGGAATCAGACGCTCTTCTGATGACCTCCCTGAATCTGATCTCT 4740  
Db 4800 ACCCTTACCTGGATCTGGAATCAGACGCTCTTCTGATGACCTCCCTGAATCTGATCTCT 4859  
QY 4741 GAAGCAGAGCCCGAGTCTGCTGCTGGGCAACATACATCTTCAACCTCTGCAATG 4800  
Db 4860 GAAGCAGAGCCCGAGTCTGCTGCTGGGCAACATACATCTTCAACCTCTGCAATG 4919  
QY 4801 AAAGTTCCCAATTTGAAGTTGCAAGATCTGCCAGGCTCCAGCTGCTGCTCATACTACT 4860  
Db 4920 AAAGTTCCCAATTTGAAGTTGCAAGATCTGCCAGGCTCCAGCTGCTGCTCATACTACT 4979  
QY 4861 GATCTGCTGGTATATGCAATGGAAGAAAGTGTGAGCAGGAGAGAGCCAGAAATGACA 4920  
Db 4980 GATCTGCTGGTATATGCAATGGAAGAAAGTGTGAGCAGGAGAGAGCCAGAAATGACA 5039  
QY 4921 GCTTCAACAGAAAGGCTCAACAAAGAAATGCTCATGCTGGTGTGCTGGCTGACCCAGAA 4980  
Db 5040 GCTTCAACAGAAAGGCTCAACAAAGAAATGCTCATGCTGGTGTGCTGGCTGACCCAGAA 5099  
QY 4981 GAATTTATGCTGCTGATCAAGTTTGCAGAAACCAACACATCACTTTAACTTAATCTAAT 5040  
Db 5100 GAATTTATGCTGCTGATCAAGTTTGCAGAAACCAACACATCACTTTAACTTAATCTAAT 5159  
QY 5041 ACTGAAGAGACTACTCATGTTGTTATGAACAAAGATGCTGAGTTGTGTGAGAGGACA 5100  
Db 5160 ACTGAAGAGACTACTCATGTTGTTATGAACAAAGATGCTGAGTTGTGTGAGAGGACA 5219  
QY 5101 CTGAATATTTCTAGGAATTTGCGGAGGAAATGGGTAGTGTAGTATTTCTGGTGACC 5160  
Db 5220 CTGAATATTTCTAGGAATTTGCGGAGGAAATGGGTAGTGTAGTATTTCTGGTGACC 5279  
QY 5161 CAGTCTATTAAGAAAGAAATGCTGAATGAGCATGTTTGAAGTCAGAGAGATGTG 5220  
Db 5280 CAGTCTATTAAGAAAGAAATGCTGAATGAGCATGTTTGAAGTCAGAGAGATGTG 5339

QY 5221 GTCAATGGAAGAAACCAAGAGTCCAAAGGTCCAAGGAGCAAGAGATCCAGGACAGAAAGATC 5280  
Db 5340 GTCAATGGAAGAAACCAAGAGTCCAAAGGTCCAAGGAGCAAGAGATCCAGGACAGAAAGATC 5399  
QY 5281 TTCAAGGGGCTAGAAAATCTGTTGCTATGAGGCGCTTCAACCAATGCGCCACAGATCAACTG 5340  
Db 5400 TTCAAGGGGCTAGAAAATCTGTTGCTATGAGGCGCTTCAACCAATGCGCCACAGATCAACTG 5459  
QY 5341 GAATGATGTTACAGCTGTGTGCTTCTGCTGAGAGAGCTTTTCATCAATTCACCTT 5400  
Db 5460 GAATGATGTTACAGCTGTGTGCTTCTGCTGAGAGAGCTTTTCATCAATTCACCTT 5519  
QY 5401 GGCAAGGTTCCACCAATTTGCTGCTGAGCAGATGCTGCAAGAGGACAATGGC 5460  
Db 5520 GGCAAGGTTCCACCAATTTGCTGCTGAGCAGATGCTGCAAGAGGACAATGGC 5579  
QY 5461 TTCCATGCAATTTGGGCGAGATGTTGAGGCGACCTGCTGCTGAGAGTGGGTGTGGAC 5520  
Db 5580 TTCCATGCAATTTGGGCGAGATGTTGAGGCGACCTGCTGCTGAGAGTGGGTGTGGAC 5639  
QY 5521 AGTGTAGCTCTTACCAAGTCCAGAGCTGGACACCTACCTGATACCCAGATCCCCAC 5580  
Db 5640 AGTGTAGCTCTTACCAAGTCCAGAGCTGGACACCTACCTGATACCCAGATCCCCAC 5699  
QY 5581 AGCCACTAC 5589  
Db 5700 AGCCACTAC 5708

RESULT 3  
ACA61333  
ID ACA61333 standard; cDNA; 5711 BP.  
XX  
AC ACA61333;  
XX  
DT 07-AUG-2003 (first entry)  
XX  
DS Human BRCA1 allele omi2, cDNA.  
XX  
KW Human; ss; gene; BRCA1; omi2; gene therapy; tumour; breast cancer;  
KW ovarian cancer; prostate cancer; colon cancer; SNP;  
KW single nucleotide polymorphism.  
XX  
OS Homo sapiens.  
XX  
Key Location/Qualifiers  
FT CDS 120..5711  
FT /\*tag= a  
FT /product= "BRCA1 omi2"  
FT allele replace(2201,C)  
FT /\*tag= b  
FT allele /note= "Single nucleotide polymorphism"  
FT replace(2430,T)  
FT /\*tag= c  
FT allele /note= "Single nucleotide polymorphism"  
FT replace(2731,C)  
FT /\*tag= d  
FT allele /note= "Single nucleotide polymorphism"  
FT replace(3232,A)  
FT /\*tag= e  
FT allele /note= "Single nucleotide polymorphism"  
FT replace(3667,A)  
FT /\*tag= f  
FT allele /note= "Single nucleotide polymorphism"  
FT replace(4427,C)  
FT /\*tag= g  
FT allele /note= "Single nucleotide polymorphism"  
FT replace(4956,A)  
FT /\*tag= h  
FT allele /note= "Single nucleotide polymorphism"  
XX  
PN US2003022184-A1.

30-JAN-2003.

22-OCT-2001; 2001US-00982828.

12-FEB-1996; 96US-00598591.

12-FEB-1997; 97US-00798691.

06-MAY-1998; 98US-00074453.

(ONCO-) ONCORMED INC.

Murphy PD., Allen ACP, Alvares CP, Critz BS, Olson SJ, Thurber D; Zeng B;

WPI; 2003-456286/43.

P-PSDB; ABU61604.

New protein sequence comprising an amino acid sequence derived from the BRCA1 omi1, omi2 or omi3 sequence useful in performing gene therapy for treating patients suspected of having tumor, e.g. breast, ovarian, prostate or colon cancer.

Claim 5; Page 25-28; 60pp; English.

The invention relates to a protein sequence comprising an amino acid sequence derived from the human BRCA1 omi1, omi2 or omi3 sequences appearing as ABU61603 ABU61605. Also included are determining the consensus genomic sequence or consensus coding sequence for a target gene, oligonucleotide probes (each capable of hybridizing to a sample BRCA1 omi gene/cDNA appearing as AC61332-AC61334) or their complements, a chip array having elements for performing allele specific sequence-based techniques comprising a solid phase chip and oligonucleotides having n different nucleotide sequences (where n is an integer greater than or equal to 7, where the oligonucleotides are bound to the solid phase chip in a manner that permits the oligonucleotides to effectively hybridize to complementary oligonucleotides or polynucleotides, and the oligonucleotides having different nucleotide sequence are bound to the solid phase chip at different locations so that a particular location on the solid phase chip exclusively binds oligonucleotides having a specific nucleotide sequence, and the oligonucleotides are capable of specifically hybridizing to the BRCA1 omi DNA), performing gene therapy on a patient, treating a patient suspected of having a tumor, a expression/cloning vector comprising the BRCA1 DNA sequence (or fragments), preventing the formation or growth of a tumor, a host cell transformed with the vector and an anti-BRCA1 antibody. The protein sequences are useful in performing gene therapy for treating patients suspected of having a tumor, e.g. breast cancer, ovarian cancer, prostate cancer or colon cancer. The antibody is useful as an immunogen. The present sequence is a cDNA representing the omi2 allele of the BRCA1 gene

Sequence 5711 BP; 1953 A; 1098 C; 1277 G; 1383 T; 0 U; 0 Other;

Query Match 100.0%; Score 5589; DB 8; Length 5711;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 5589; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ATGGATTATCTGCTCTTCGGGTTGAAGAGTACAAATGTCATTATGCTATGTCAGAAA 60

120 ATGGATTATCTGCTCTTCGGGTTGAAGAGTACAAATGTCATTATGCTATGTCAGAAA 179

61 ATCTTAGAGTGTCCATCTGTCTGGAGTTGATCAAGGAACCTGTCTCCACAAAGTGTGAC 120

180 ATCTTAGAGTGTCCATCTGTCTGGAGTTGATCAAGGAACCTGTCTCCACAAAGTGTGAC 239

121 CACATATTTGCAAAATTTGCATGCTGAACCTTCTCAACAGAAAGAGGCGCTTCACAG 180

240 CACATATTTGCAAAATTTGCATGCTGAACCTTCTCAACAGAAAGAGGCGCTTCACAG 299

181 TGTCTTTATGTAGATGATATACCAAAAGGAGGCTTACAAAGATACAGATTAGT 240

300 TGTCTTTATGTAGATGATATACCAAAAGGAGGCTTACAAAGATACAGATTAGT 359

241 CAACTTGTTGAAGAGCTATTGAAAATCATTTTGCTTTTCAGCTTGTGACACAGGTTGGAG 300

Db 360 CAACCTTGTGAAGAGCTATTGAAAATCATTTTGGCTTTTCAGCTTGAACAGGTTTGGAG 419

Qy 301 TATGCAAAACAGCTATATATTTTGCAGAAAAGGAAAAATAACTCTCTCTGAACATCTAAAAGAT 360

Db 420 TATGCAAAACAGCTATATATTTTGCAGAAAAGGAAAAATAACTCTCTCTGAACATCTAAAAGAT 479

Qy 361 GAAGTTTCTATCATCCAAAGTATGGGCTACAGAAAACGTCGCGCAAAAGACTTCTACAGAGT 420

Db 480 GAAGTTTCTATCATCCAAAGTATGGGCTACAGAAAACGTCGCGCAAAAGACTTCTACAGAGT 539

Qy 421 GAACCCGAAAATCTCTCTTTCAGAGGAAAACAGCTCTCAGTGTCCAACTCTCTAAACCTTGGGA 480

Db 540 GAACCCGAAAATCTCTCTTTCAGAGGAAAACAGCTCTCAGTGTCCAACTCTCTAAACCTTGGGA 599

Qy 481 ACTGTGAGAACTCTGAGGACAAAAGCAGCGGATACAACTCAAAAGAGCTGTGTCTACATT 540

Db 600 ACTGTGAGAACTCTGAGGACAAAAGCAGCGGATACAACTCAAAAGAGCTGTGTCTACATT 659

Qy 541 GAATTTGGGATCTGATTTCTCTGAAGATACCGTTTAATAAGCAACTTATTTCAGTGTGGGA 600

Db 660 GAATTTGGGATCTGATTTCTCTGAAGATACCGTTTAATAAGCAACTTATTTCAGTGTGGGA 719

Qy 601 GATCAAGAAATGTTTACAAATCACCCCTCAAGGAACAGGAGTCAAAATCAGTTTGGATTCT 660

Db 720 GATCAAGAAATGTTTACAAATCACCCCTCAAGGAACAGGAGTCAAAATCAGTTTGGATTCT 779

Qy 661 GCAGAAAAGGCTCTGTTGTAATTTCTGAGACCGGATGTAACAAATCTGAGCAATCTCAAA 720

Db 780 GCAGAAAAGGCTCTGTTGTAATTTCTGAGACCGGATGTAACAAATCTGAGCAATCTCAAA 839

Qy 721 CCAGTAATAATGATTTGAACACCACTGAGAGCGTGCAGCTGAGAGGAGTCCAGAAAAG 780

Db 840 CCAGTAATAATGATTTGAACACCACTGAGAGCGTGCAGCTGAGAGGAGTCCAGAAAAG 839

Qy 781 TATCAGGAGTGTCTGTTTCAAACTGCTGCTGAGGCGCATGTGGCAAAATCTCATGCC 840

Db 900 TATCAGGAGTGTCTGTTTCAAACTGCTGCTGAGGCGCATGTGGCAAAATCTCATGCC 959

Qy 841 AGCTCATTTACAGCATGAGAACAGCAGTTTATTACTCACTAAAAGACAGAAATGATGAGAA 900

Db 960 AGCTCATTTACAGCATGAGAACAGCAGTTTATTACTCACTAAAAGACAGAAATGATGAGAA 1019

Qy 901 AAGGCTGAATTTCTGTAATAAAGCAAAAGCCTGCTTGAAGAGGAGCAAAATACACAGA 960

Db 1020 AAGGCTGAATTTCTGTAATAAAGCAAAAGCCTGCTTGAAGAGGAGCAAAATACACAGA 1079

Qy 961 TGGGCTGGAAGTAAGGAACATGTAATGATAGCGGACTCCAGACACAGAAAAGGTA 1020

Db 1080 TGGGCTGGAAGTAAGGAACATGTAATGATAGCGGACTCCAGACACAGAAAAGGTA 1139

Qy 1021 GATCTGAATGCTGATCCCTGTTGAGAGAAAGAAATGGAATAGCAGAAAACCTGCCATCC 1080

Db 1140 GATCTGAATGCTGATCCCTGTTGAGAGAAAGAAATGGAATAGCAGAAAACCTGCCATCC 1199

Qy 1081 TCAGAGAAATCTTAGAGATACAGAGTGTCTCTTGATTAACACTAAATAGCAGGCTTCAG 1140

Db 1200 TCAGAGAAATCTTAGAGATACAGAGTGTCTCTTGATTAACACTAAATAGCAGGCTTCAG 1259

Qy 1141 AAAGTTAATAGAGTGGTGTTCAGAGAAAGTGAATGATGTTTGGTTCCTGATGACTCAATGAT 1200

Db 1260 AAAGTTAATAGAGTGGTGTTCAGAGAAAGTGAATGATGTTTGGTTCCTGATGACTCAATGAT 1319

Qy 1201 GGGGAGTCTGAATCAAAATCCCAAGTAGCTGATGTTATTTGGAGTTCTTAATAGGAGTAGAT 1260

Db 1320 GGGGAGTCTGAATCAAAATCCCAAGTAGCTGATGTTATTTGGAGTTCTTAATAGGAGTAGAT 1379

Qy 1261 GAATATTCTGGTTCCTTCAGAGAAAATAGACTTACTTGGGCGAGTGTCTCTCAGGCGTTTA 1320

Db 1380 GAATATTCTGGTTCCTTCAGAGAAAATAGACTTACTTGGGCGAGTGTCTCTCAGGCGTTTA 1439

Qy 1321 ATATGTAAAGTGAAGAGTTCACCTCCAAATCAGTAGAGAGTAAATATTGAAAGACAAAATA 1380



1440	DB	ATA	GT	ATAAAGTG	AAAGAG	TTCACTCCAAATCAGT	AGAGTAATA	TTG	AGACA	CAAAATA	1449															
1381	QY	TTTGG	AAAA	CTTATCG	GAAGAGCG	CAAGCCTCC	CCAACTTAA	AGC	ATGAA	CTG	AAAAAT	1440														
1500	DB	TTTGG	AAAA	CTTATCG	GAAGAGCG	CAAGCCTCC	CCAACTTAA	AGC	ATGAA	CTG	AAAAAT	1559														
1441	QY	CTA	ATTATAG	AGCA	NTTGT	TACTG	AGCCACAG	ATATATA	CAAG	AGCGT	CCCTC	CAAAAT	1500													
1560	DB	CTA	ATTATAG	AGCA	NTTGT	TACTG	AGCCACAG	ATATATA	CAAG	AGCGT	CCCTC	CAAAAT	1619													
1501	QY	AAA	TTAAAG	CGTAAA	AGGAGAC	CTACATC	AGGCGCTT	CATCTG	TAGG	ATTTTAT	CAAGAAA	1560														
1620	DB	AAA	TTAAAG	CGTAAA	AGGAGAC	CTACATC	AGGCGCTT	CATCTG	TAGG	ATTTTAT	CAAGAAA	1679														
1561	QY	GC	AGATTTGG	CGAGTTC	AAAAAG	CTCTG	GAATAT	ATATAT	CAGG	AAATAC	CAACCGG	AG	1620													
1680	DB	GC	AGATTTGG	CGAGTTC	AAAAAG	CTCTG	GAATAT	ATATAT	CAGG	AAATAC	CAACCGG	AG	1739													
1621	QY	CAG	AATGGT	CAAGT	GTATCA	ATATTA	CTAATAG	TGGT	CATG	AGATATA	AAAA	CAAAAG	GTAT	1680												
1740	DB	CAG	AATGGT	CAAGT	GTATCA	ATATTA	CTAATAG	TGGT	CATG	AGATATA	AAAA	CAAAAG	GTAT	1799												
1681	QY	TCT	ATT	CAGA	ATG	AAAAAT	CTCTA	AGCC	ATATAG	AAATCA	CTCTG	AAAAA	AGATCTG	CTTTC	1740											
1800	DB	TCT	ATT	CAGA	ATG	AAAAAT	CTCTA	AGCC	ATATAG	AAATCA	CTCTG	AAAAA	AGATCTG	CTTTC	1859											
1741	QY	AAA	ACG	AAAG	CGTGA	ACCTTA	AGC	AGCAG	TATATAG	CAATAT	TGGA	ACCTT	CGA	ATTTAA	ATATC	1800										
1860	DB	AAA	ACG	AAAG	CGTGA	ACCTTA	AGC	AGCAG	TATATAG	CAATAT	TGGA	ACCTT	CGA	ATTTAA	ATATC	1919										
1801	QY	CAC	AATTC	CAAA	AGCA	CTCTA	AAAA	AGAA	TAG	CGT	TGAG	AGG	AA	GTCTTCT	CA	CCAG	CAATAT	1860								
1920	DB	CAC	AATTC	CAAA	AGCA	CTCTA	AAAA	AGAA	TAG	CGT	TGAG	AGG	AA	GTCTTCT	CA	CCAG	CAATAT	1979								
1861	QY	CAT	CGCTTGA	ACTAG	TAGT	CACTAG	AAAA	CTTA	AGCC	CACTTA	TTGT	TGT	ACT	GA	ATTTG	CA	ATG	CA	1920							
1980	DB	CAT	CGCTTGA	ACTAG	TAGT	CACTAG	AAAA	CTTA	AGCC	CACTTA	TTGT	TGT	ACT	GA	ATTTG	CA	ATG	CA	2039							
1921	QY	ATT	GATAGT	TTCT	TAG	CAGTGA	AGAGAT	AAAG	AAAA	AAAAA	AGTAC	AAAC	CAAA	TGCC	AGT	C	1980									
2040	DB	ATT	GATAGT	TTCT	TAG	CAGTGA	AGAGAT	AAAG	AAAA	AAAAA	AGTAC	AAAC	CAAA	TGCC	AGT	C	2099									
1981	QY	AGG	CAC	AGC	AG	CAAA	ACTTA	CA	CTG	GAAG	GTAAA	GA	AACTG	CA	CTG	AG	AG	CA	2040							
2100	DB	AGG	CAC	AGC	AG	CAAA	ACTTA	CA	CTG	GAAG	GTAAA	GA	AACTG	CA	CTG	AG	AG	CA	2159							
2041	QY	AGT	AAC	AGC	CA	AAATGA	ACAC	AG	GTAAA	AG	CA	CTG	AG	GTG	ATAT	CTTTCC	AG	AG	CTG	2100						
2160	DB	AGT	AAC	AGC	CA	AAATGA	ACAC	AG	GTAAA	AG	CA	CTG	AG	GTG	ATAT	CTTTCC	AG	AG	CTG	2219						
2101	QY	AAG	TTAA	CAAA	TG	CAC	CTGG	TTCTTT	TCTA	AGT	GTTC	CA	ATAT	CC	AGT	GA	ACTTT	TA	AG	2160						
2220	DB	AAG	TTAA	CAAA	TG	CAC	CTGG	TTCTTT	TCTA	AGT	GTTC	CA	ATAT	CC	AGT	GA	ACTTT	TA	AG	2279						
2161	QY	TTT	GT	CTA	ATCT	TAG	CGCTTCC	AG	GA	GA	AAAG	AG	AG	AA	CTAG	AAA	CAG	TTA	AG	CTG	2220					
2280	DB	TTT	GT	CTA	ATCT	TAG	CGCTTCC	AG	GA	GA	AAAG	AG	AG	AA	CTAG	AAA	CAG	TTA	AG	CTG	2339					
2221	QY	TCT	ATA	TAAT	TG	CT	GAAG	CCCC	CA	AA	AG	ATCT	CAT	GT	TTA	AG	TG	TG	AG	AAAG	GG	TTTT	TG	CAAA	CT	2280
2340	DB	TCT	ATA	TAAT	TG	CT	GAAG	CCCC	CA	AA	AG	ATCT	CAT	GT	TTA	AG	TG	TG	AG	AAAG	GG	TTTT	TG	CA		

QY	2461	GATTAATAGAAATGACACAGAAAGGCTTTAAAGTATCCATTTGGGCATCGAAGTTTAAACCAACGTT	2520
DB	2580	GATTAATAGAAATGACACAGAAAGGCTTTAAAGTATCCATTTGGGCATCGAAGTTTAAACCAACGTT	2639
QY	2521	CGGGAACCAAGCATAGAAATGGAAGAAAGTGAACCTTGATGCTCAGTATTTGCGAGAATACA	2580
DB	2640	CGGGAACCAAGCATAGAAATGGAAGAAAGTGAACCTTGATGCTCAGTATTTGCGAGAATACA	2699
QY	2581	TTCAAGGTTTCAAGGCGCCAGTCATTTGCTCTGTTTTCAATCCAGGAATCGCAAGAG	2640
DB	2700	TTCAAGGTTTCAAGGCGCCAGTCATTTGCTCTGTTTTCAATCCAGGAATCGCAAGAG	2759
QY	2641	GAATGTGCAACATTTCTCTGCGCCACTCTGGGTCCTTTAAAGAAAAAAAAGTCCAAAGTCACT	2700
DB	2760	GAATGTGCAACATTTCTCTGCGCCACTCTGGGTCCTTTAAAGAAAAAAAAGTCCAAAGTCACT	2819
QY	2701	TTTGAATGTGACAAAGGAAGAAATCAAGGAAGAAATGAAGTCTTAATATCAAGCCCTGTA	2760
DB	2820	TTTGAATGTGACAAAGGAAGAAATCAAGGAAGAAATGAAGTCTTAATATCAAGCCCTGTA	2879
QY	2761	CAGACAGTTAATATCACTGCGAGGCTTTCTCTGTGTGGTCAGAAAGATGAAGCCAGTTGAT	2820
DB	2880	CAGACAGTTAATATCACTGCGAGGCTTTCTCTGTGTGGTCAGAAAGATGAAGCCAGTTGAT	2939
QY	2821	AATGCCAAATGTAGTATCAAGGAGGCTCTAGGTTTTGTCTATCATCTCAGTTCAGAGGC	2880
DB	2940	AATGCCAAATGTAGTATCAAGGAGGCTCTAGGTTTTGTCTATCATCTCAGTTCAGAGGC	2999
QY	2881	AACGAAACTTGGACTCATTTACTCCAAATFAAACATGGACTTTTTTACAAACCCTATCGTATA	2940
DB	3000	AACGAAACTTGGACTCATTTACTCCAAATFAAACATGGACTTTTTTACAAACCCTATCGTATA	3059
QY	2941	CCACCACTTTTCCCATCAAGTCACTGTGTGTTAAACCTAAATGTGAAGAAATCTGCTAGAG	3000
DB	3060	CCACCACTTTTCCCATCAAGTCACTGTGTGTTAAACCTAAATGTGAAGAAATCTGCTAGAG	3119
QY	3001	GAAGAACTTTGAGGAACATTCAAATGTCACCTGGAAGAGAAATGGGAATGAGAACATTCCA	3060
DB	3120	GAAGAACTTTGAGGAACATTCAAATGTCACCTGGAAGAGAAATGGGAATGAGAACATTCCA	3179
QY	3061	AGTACAGTGAGCAAAATAGCCGCTATATACATTTAGAGAAATGTTTTTAAAGGCGCAGC	3120
DB	3180	AGTACAGTGAGCAAAATAGCCGCTATATACATTTAGAGAAATGTTTTTAAAGGCGCAGC	3239
QY	3121	TCAAGCAATATTAAATGAAGTAGTTCACGACTCAATGAAGTGGGCTCCAGTTAATGAATGAA	3180
DB	3240	TCAAGCAATATTAAATGAAGTAGTTCACGACTCAATGAAGTGGGCTCCAGTTAATGAATGAA	3299
QY	3181	ATAGGTTCCAGTGAATGAACATTTCAAGCAGACTAGGTAGAAACAGAGGCGCAAAATTTG	3240
DB	3300	ATAGGTTCCAGTGAATGAACATTTCAAGCAGACTAGGTAGAAACAGAGGCGCAAAATTTG	3359
QY	3241	AATGCTATGCTTAGATTAGGGGTTTTGCAACCTGAGGTCCTATAAAACAAAGTCTTCTCGA	3300
DB	3360	AATGCTATGCTTAGATTAGGGGTTTTGCAACCTGAGGTCCTATAAAACAAAGTCTTCTCGA	3419
QY	3301	AGTAATTTGAAGCATCTCGAAATATAAAACAGCAAGATATCAAGAGTAGTTCAGACTGTT	3360
DB	3420	AGTAATTTGAAGCATCTCGAAATATAAAACAGCAAGATATCAAGAGTAGTTCAGACTGTT	3479
QY	3361	AATACAGATTTCTTCCATATCTGATTTTCAGATTAATTTAGAACAGCCTTATGGGAAGTAGT	3420
DB	3480	AATACAGATTTCTTCCATATCTGATTTTCAGATTAATTTAGAACAGCCTTATGGGAAGTAGT	3539
QY	3421	CATGCACTTCAGGTTTTGCTTCGAGACACCTGATGACCTGTTAGATCATGCTGGAATAAAG	3480
DB	3540	CATGCACTTCAGGTTTTGCTTCGAGACACCTGATGACCTGTTAGATCATGCTGGAATAAAG	3599
QY	3481	GAAGATACTAGTTTTGCTTGAATAATGAATTAAGGAAGTCTTGCTTTTTTATAGCAAAAC	3540
DB	3600	GAAGATACTAGTTTTGCTTGAATAATGAATTAAGGAAGTCTTGCTTTTTTATAGCAAAAC	3659

3541 GTCCAGAGAGGAGCTTAGCAGAGTCTAGCCCTTTACCCATACATTTGGCTCAG 3600  
3660 GTCCAGAGAGGAGCTTAGCAGAGTCTAGCCCTTTACCCATACATTTGGCTCAG 3719  
3601 GGTACCCAGAGGGGCCAAGAAATTAGAGTCTCAGAGAGAACTTATCTAGTGCAGAT 3660  
3720 GGTACCCAGAGGGGCCAAGAAATTAGAGTCTCAGAGAGAACTTATCTAGTGCAGAT 3779  
3661 GAAGAGCTTCCCTGCTTCCAAACACTTGTATTTGGTAAAGTAAACAATATACCTTCTCAG 3720  
3780 GAAGAGCTTCCCTGCTTCCAAACACTTGTATTTGGTAAAGTAAACAATATACCTTCTCAG 3839  
3721 TCTACTAGCATAGCAGCTGCTACCGAGTGTCTCTTAAGAACACAGAGAGAAATTTA 3780  
3840 TCTACTAGCATAGCAGCTGCTACCGAGTGTCTCTTAAGAACACAGAGAGAAATTTA 3899  
3781 TTATCAATGAAGAAATAGCTTAAATGACTGCAAGTAAACAGAGTAAATTTGGCAAGGCATCT 3840  
3900 TTATCAATGAAGAAATAGCTTAAATGACTGCAAGTAAACAGAGTAAATTTGGCAAGGCATCT 3959  
3841 CAGGAACATCAGCTTAGTGAGGAAACAAATGTTCTGCTAGCTTGTCTTCTCAGAGTGC 3900  
3960 CAGGAACATCAGCTTAGTGAGGAAACAAATGTTCTGCTAGCTTGTCTTCTCAGAGTGC 4019  
3901 AGTGAATTTGGAAGACTTGAATGCAATACAAACACCCAGGATCCTTTCTCAATGGTCT 3960  
4020 AGTGAATTTGGAAGACTTGAATGCAATACAAACACCCAGGATCCTTTCTCAATGGTCT 4079  
3961 TCCAAACAAATAGAGGCATCAGTCTGAAGACAGAGGAGTGTCTGAGTGAACAAGAAATG 4020  
4080 TCCAAACAAATAGAGGCATCAGTCTGAAGACAGAGGAGTGTCTGAGTGAACAAGAAATG 4139  
4021 GTTTCAGATGATGAAGAAAGAGGAAACGGCTTGAAGAAATATCAAGAGAGCAAGAC 4080  
4140 GTTTCAGATGATGAAGAAAGAGGAAACGGCTTGAAGAAATATCAAGAGAGCAAGAC 4199  
4081 ATGGAATCAAACTTAGTGGAAGCAGCTCTGGGTGTGAGAGTGAAGAAACGGCTCTCGAA 4140  
4200 ATGGAATCAAACTTAGTGGAAGCAGCTCTGGGTGTGAGAGTGAAGAAACGGCTCTCGAA 4259  
4141 GACTGCTCAGGGCTATCCTCTCAGAGTGAACATTTTAAACCTCAGCAGAGGATACCATG 4200  
4260 GACTGCTCAGGGCTATCCTCTCAGAGTGAACATTTTAAACCTCAGCAGAGGATACCATG 4319  
4201 CAACATACCTGTATAAGCTCCAGAGAAATGCTGAACTAGAGTGTGTAGAAACAG 4260  
4320 CAACATACCTGTATAAGCTCCAGAGAAATGCTGAACTAGAGTGTGTAGAAACAG 4379  
4261 CATGGAGCCAGCTCTTAACAGCTTACCTTCCATCATATAGTGACTCTTCTGCCCTTGAG 4320  
4380 CATGGAGCCAGCTCTTAACAGCTTACCTTCCATCATATAGTGACTCTTCTGCCCTTGAG 4439  
4321 GACTGCGAAATCCAGAAACAAAGCACATCAGAAAGCAGTATTAACCTTCAAGAAAGT 4380  
4440 GACTGCGAAATCCAGAAACAAAGCACATCAGAAAGCAGTATTAACCTTCAAGAAAGT 4499  
4381 AGTCAATACCTTAAAGCCAGAAATCCAGAGGCTTCTTCTGTCAGAGTGTAGGTGTCT 4440  
4500 AGTCAATACCTTAAAGCCAGAAATCCAGAGGCTTCTTCTGTCAGAGTGTAGGTGTCT 4559  
4441 GCAGATAGTCTTACAGTAAATAAAGAACACAGAGTGAAGGTCATGCCCTTCTAAA 4500  
4560 GCAGATAGTCTTACAGTAAATAAAGAACACAGAGTGAAGGTCATGCCCTTCTAAA 4619  
4501 TGCCCATCATATAGTATAGTGTGTAATGCAAGTGTCTTGGAGTCTTTCAGATAGA 4560  
4620 TGCCCATCATATAGTATAGTGTGTAATGCAAGTGTCTTGGAGTCTTTCAGATAGA 4679  
4561 AACTTACCATCTCAAGAGGAGCTCAATTAAGTGTCTGATGTGGAGGACACAGCTGGAA 4620  
4680 AACTTACCATCTCAAGAGGAGCTCAATTAAGTGTCTGATGTGGAGGAGACAGCTGGAA 4739  
4621 GAGTCTGGGCCACACAGATTTGACGGAAACATCTTACTTGGCCAAAGCAAGATCTAGAGGGA 4680

4740 GAGTCTGGGCCACACAGATTTGACGGAAACATCTTACTTGCAGGCAAGATCTAGAGGA 4799  
4681 ACCCTTACCTTGAATCTGGAATCAGCCTCTTCTCTGATGACCTGAATCTGATCTCT 4740  
4800 ACCCTTACCTTGAATCTGGAATCAGCCTCTTCTCTGATGACCTGAATCTGATCTCT 4859  
4741 GAAGACAGAGCCCGAGAGTCACTGCTGTTGGCAACATACCATCTTCAACCTCTGCATTG 4800  
4860 GAAGACAGAGCCCGAGAGTCACTGCTGTTGGCAACATACCATCTTCAACCTCTGCATTG 4919  
4801 AAAGTCTCCCAATTTGAAGTTGCAAGATCTGCCAGGTCAGCTGCTGCTCACTACT 4860  
4920 AAAGTCTCCCAATTTGAAGTTGCAAGATCTGCCAGGTCAGCTGCTGCTCACTACT 4979  
4861 GATACTGCTGGGTATTAATGCAATGGAAGAAAGTGTGACGAGGAGGAAGCCAGAAATGACA 4920  
4980 GATACTGCTGGGTATTAATGCAATGGAAGAAAGTGTGACGAGGAGGAAGCCAGAAATGACA 5039  
4921 GCTTCAACAGAGAGGGTCAACAAAGAAATGTCATGCTGGTGTCTGGCTGACCCAGAA 4980  
5040 GCTTCAACAGAGAGGGTCAACAAAGAAATGTCATGCTGGTGTCTGGCTGACCCAGAA 5099  
4981 GAATTTATGCTGCTGACAAAGTTTGGCAGAAACACACATCACTTTAACTTAAT 5040  
5100 GAATTTATGCTGCTGACAAAGTTTGGCAGAAACACACATCACTTTAACTTAAT 5159  
5041 ACTGAGAGAGTACTACTGCTGTTATTAAGAAACAGATGCTGAGTTGTGTGAAACGACA 5100  
5160 ACTGAGAGAGTACTACTGCTGTTATTAAGAAACAGATGCTGAGTTGTGTGAAACGACA 5219  
5101 CTCAAAATATTTCTAGCAATTTGGCAGGAAATGCTGATGCTAGTATTTCTGGGTGACC 5160  
5220 CTCAAAATATTTCTAGCAATTTGGCAGGAAATGCTGATGCTAGTATTTCTGGGTGACC 5279  
5161 CAGTCTATTAAAGAAAGAAATGCTGATGCTAGTATTTGAAAGTCAAGAGAGATGTG 5220  
5280 CAGTCTATTAAAGAAAGAAATGCTGATGCTAGTATTTGAAAGTCAAGAGAGATGTG 5339  
5221 GTCAATGGAAGAAACCAACCAAGGTCAGAGCAAGAGAAATCCAGAGACAGAAAGATC 5280  
5340 GTCAATGGAAGAAACCAACCAAGGTCAGAGCAAGAGAAATCCAGAGACAGAAAGATC 5399  
5281 TTCAAGGGGCTAGAAATCTGTTGCTATGCGCCCTTCCAAACATGCCACAGATCAACTG 5340  
5400 TTCAAGGGGCTAGAAATCTGTTGCTATGCGCCCTTCCAAACATGCCACAGATCAACTG 5459  
5341 GAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5400  
5460 GAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5519  
5401 GGCAAGGTGTCCACCAATTTGTTGTTGTCAGCCAGATGCTGTCAGAGAGCAATGGC 5460  
5520 GGCAAGGTGTCCACCAATTTGTTGTTGTCAGCCAGATGCTGTCAGAGAGCAATGGC 5579  
5461 TTCCATGCAATTTGGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5520  
5580 TTCCATGCAATTTGGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5639  
5521 AGTGTAGCACTCTTACAGTCCAGAGGAGTGTGAGCACTTACTGATATCCAGAGATCCCCC 5580  
5640 AGTGTAGCACTCTTACAGTCCAGAGGAGTGTGAGCACTTACTGATATCCAGAGATCCCCC 5699  
5581 AGCCACTAC 5589  
5700 AGCCACTAC 5708

RESULT 4

AD63291

ID AD63291 standard; cDNA; 571i BP.

XX

AC AD63291;

XX 18-DEC-2003 (first entry)  
XX Polymorphic cDNA sequence (om13) for human BRCA1.  
XX Human; BRCA1; om13; gene pool; gene therapy; BRCA1 gene mutation;  
XX breast cancer; ovarian cancer; cytostatic; chromosome 17q21; gene; ss.  
XX Homo sapiens.  
XX US2002183268-A1.  
XX 05-DEC-2002.  
XX 13-DEC-2000; 2000US-00734672.  
XX 12-FEB-1996; 96US-00598591.  
XX 07-NOV-1997; 97US-00966436.  
XX (MURP/) MURPHY P. D.  
XX (ALLEN/) ALLEN A. C.  
XX (ALVA/) ALVARES C. P.  
XX (CRIT/) CRITZ B. S.  
XX (OLSO/) OLSON S. J.  
XX (SCHE/) SCHELTER D. B.  
XX (ZENG/) ZENG B.  
XX Murphy PD., Allen AC, Alvares CP, Critz BS, Olson SJ, Schelter DB;  
XX Zeng B;  
XX WPI; 2003-765230/72.  
XX P-PSDB; ADC63292.  
XX New isolated DNA sequence of the BRCA1 coding sequence, useful for the  
XX diagnosis and treatment of disorders with BRCA1 gene mutation, such as  
XX breast and ovarian cancer.  
XX Claim 5; SEQ ID NO 5; 59pp; English.  
XX The present invention relates to the isolation of a consensus DNA  
XX sequence of the human BRCA1 coding sequence (om11), and two polymorphic  
XX coding sequences for human BRCA1 (om12 and om13). The gene encoding human  
XX BRCA1 maps to chromosome 17q21. Also disclosed are the three proteins  
XX encoded by these polynucleotide sequences, and a method of determining  
XX the consensus sequence for BRCA1. Om11 represents the most commonly  
XX occurring coding sequence in the human gene pool. The coding sequences  
XX are useful for gene therapy and can be administered by direct injection  
XX into the tissue. The methods and compositions of the present invention  
XX are useful for the diagnosis and treatment of disorders with BRCA1 gene  
XX mutations, such as breast and ovarian cancer. The present sequence  
XX represents a polymorphic cDNA sequence for human BRCA1.  
XX  
XX Sequence 5711 BP; 1953 A; 1098 C; 1277 G; 1383 T; 0 U; 0 Other;  
Query Match 100.0%; Score 5589; DB 9; Length 5711;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 5589; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ATGGATTATCTGCTCTCTGCGTTGAGAGAGTACAAATGTCATTAATGCTATGACAGAA 60  
DB 120 ATGGATTATCTGCTCTCTGCGTTGAGAGAGTACAAATGTCATTAATGCTATGACAGAA 179  
QY 61 ATCTTAGAGTGTCCTCTCTGCGTTGAGAGAGTACAAATGTCATTAATGCTATGACAGAA 120  
DB 180 ATCTTAGAGTGTCCTCTCTGCGTTGAGAGAGTACAAATGTCATTAATGCTATGACAGAA 239  
QY 121 CACATATTTTGAATTTTTCATGCTGAACTTCTCAACAGAGAGAGGCGCTTCACAG 180  
DB 240 CACATATTTTGAATTTTTCATGCTGAACTTCTCAACAGAGAGAGGCGCTTCACAG 299  
QY 181 TGCTCTTTATGTAAGATGATATAACCAAAAGAGAGGCGCTTACAGAAAGTACGAGATTAGT 240  
DB 300 TGCTCTTTATGTAAGATGATATAACCAAAAGAGAGGCGCTTACAGAAAGTACGAGATTAGT 359

QY 241 CAACCTTTGAGAGAGCTATTGAAATCATTTGTGCTTTTTCAGCTTGCACAGGTTGGAG 300  
DB 360 CAACCTTTGAGAGAGCTATTGAAATCATTTGTGCTTTTTCAGCTTGCACAGGTTGGAG 419  
QY 301 TATGCAAAACAGCTATTAATTTTGCAAAAGAGAAATAAATCTCTCTGCAACATCTAAAGAT 360  
DB 420 TATGCAAAACAGCTATTAATTTTGCAAAAGAGAAATAAATCTCTCTGCAACATCTAAAGAT 479  
QY 361 GAAGTTTCTATCATCCAAAGTATGGCTACAGAAACCGTCCCAAAAGAGCTTCTACAGAGT 420  
DB 480 GAAGTTTCTATCATCCAAAGTATGGCTACAGAAACCGTCCCAAAAGAGCTTCTACAGAGT 539  
QY 421 GAAACCCGAAATCCCTTCTTTCAGGAAACCAAGTCTCAGTGTCCAACTCTCTAACTTGGGA 480  
DB 540 GAAACCCGAAATCCCTTCTTTCAGGAAACCAAGTCTCAGTGTCCAACTCTCTAACTTGGGA 599  
QY 481 ACTGTGAGAACTCTGAGGACCAAGCAGCGATACAACTCTCAAGAGAGCTGTCTCATATT 540  
DB 600 ACTGTGAGAACTCTGAGGACCAAGCAGCGATACAACTCTCAAGAGAGCTGTCTCATATT 659  
QY 541 GAAATGCGATCTGATTCTTCTGAAGATACCGTTTAAATAGGCAACTTATTGCACTGTGGGA 600  
DB 660 GAAATGCGATCTGATTCTTCTGAAGATACCGTTTAAATAGGCAACTTATTGCACTGTGGGA 719  
QY 601 GATCAGAAATTTGTTACAAATCACCCCTCAAGGACCGGATGAAATCAAGTCTTGGATTCT 660  
DB 720 GATCAGAAATTTGTTACAAATCACCCCTCAAGGACCGGATGAAATCAAGTCTTGGATTCT 779  
QY 661 GCACAAAAGGCTGCTTGTGAAATTTTCTGAGACGAGTGTAACTAACTAACTAACTAACTAA 720  
DB 780 GCACAAAAGGCTGCTTGTGAAATTTTCTGAGACGAGTGTAACTAACTAACTAACTAACTAA 839  
QY 721 CCCAGTAATTAATGATTGTAACACCACTGAGAGACGCTGACAGTGTGAGAGGATCCAGAAAG 780  
DB 840 CCCAGTAATTAATGATTGTAACACCACTGAGAGACGCTGACAGTGTGAGAGGATCCAGAAAG 899  
QY 781 TATCAGGAGTGTCTGTTTCAAACTTGCATGTGAGGACCATGTGGCAAAATCTCATGCC 840  
DB 900 TATCAGGAGTGTCTGTTTCAAACTTGCATGTGAGGACCATGTGGCAAAATCTCATGCC 959  
QY 841 AGCTCATTAACAGCATGAGAACGAGCTTTTATTACTACTTAAAGACAGAAATGATGTAGAA 900  
DB 960 AGCTCATTAACAGCATGAGAACGAGCTTTTATTACTACTTAAAGACAGAAATGATGTAGAA 1019  
QY 901 AAGCGTGAATTTCTGTAATTAAGCAACAGCCTGCTTAGCAAGGAGCCACATACAGA 960  
DB 1020 AAGCGTGAATTTCTGTAATTAAGCAACAGCCTGCTTAGCAAGGAGCCACATACAGA 1079  
QY 961 TGGGCTGGAAGTAAAGGAAACATGTATATGATAGGCGGACTCCCGAGCAGAGAAAAAGGTA 1020  
DB 1080 TGGGCTGGAAGTAAAGGAAACATGTATATGATAGGCGGACTCCCGAGCAGAGAAAAAGGTA 1139  
QY 1021 GATCTGAATGCTGATCCCTGCTGTGAGAGAAAGATGGAATAGGAGAGAACTGCCATGC 1080  
DB 1140 GATCTGAATGCTGATCCCTGCTGTGAGAGAAAGATGGAATAGGAGAGAACTGCCATGC 1199  
QY 1081 TCAGAGAACTCTAGAGATCTCAAGATGTTCTTGGATAACTAACTAACTAGCAGCATTCAG 1140  
DB 1200 TCAGAGAACTCTAGAGATCTCAAGATGTTCTTGGATAACTAACTAACTAGCAGCATTCAG 1259  
QY 1141 AAGTTTAAATGATGTTGTTTCCAGAGTGTATGAACTGTTAGGTTCTGATGATCAATGAT 1200  
DB 1260 AAGTTTAAATGATGTTGTTTCCAGAGTGTATGAACTGTTAGGTTCTGATGATCAATGAT 1319  
QY 1201 GGGGAGTCTGAATCAAAATGCCAAAGTGTATGAGAGTGTATGAGAGTGTCTTAATGAGGTAGT 1260  
DB 1320 GGGGAGTCTGAATCAAAATGCCAAAGTGTATGAGAGTGTATGAGAGTGTCTTAATGAGGTAGT 1379  
QY 1261 GAATATTTCTGTTTCTTTCAGAGAAATAGACTTACTGGCCAGTGTCTCATGAGGCTTTA 1320  
DB 1380 GAATATTTCTGTTTCTTTCAGAGAAATAGACTTACTGGCCAGTGTCTCATGAGGCTTTA 1439

1321 ATATGTAAGTAAAGAGTTCCTCCAAATCAGTAGAGTAATATTAAGACAAAATA 1380  
1440 ATATGTAAGTAAAGAGTTCCTCCAAATCAGTAGAGTAATATTAAGACAAAATA 1499  
1381 TTGCGGAAAACCTATCGGAAGAGCAAGCCCTCCCAACTTAAGCCATGTAACGAAAT 1440  
1500 TTGCGGAAAACCTATCGGAAGAGCAAGCCCTCCCAACTTAAGCCATGTAACGAAAT 1559  
1441 CTAATTAATAGGACATTTGTTACTAGCAGCCACAGATAAATACAAAGCGTCCCTCACAAAT 1500  
1560 CTAATTAATAGGACATTTGTTACTAGCAGCCACAGATAAATACAAAGCGTCCCTCACAAAT 1619  
1501 AAAATTAAGCGTAAAGGAGACCTACATCAGCCCTTCATCTCGAGGATTTTATCAAGAAA 1560  
1620 AAAATTAAGCGTAAAGGAGACCTACATCAGCCCTTCATCTCGAGGATTTTATCAAGAAA 1679  
1561 CGAGATTTGCGGATTTCAAGAGCTCCTGAAATGATAAATCAGGGAATCAACAAACGAG 1620  
1680 CGAGATTTGCGGATTTCAAGAGCTCCTGAAATGATAAATCAGGGAATCAACAAACGAG 1739  
1621 CAGAAATGATGATGAATTAATTAATAGTGTCTCATGGAATTAACAAAGGTTGAT 1680  
1740 CAGAAATGATGATGAATTAATTAATAGTGTCTCATGGAATTAACAAAGGTTGAT 1799  
1681 TCTATTCAGATGAGAAAATCCTTAACCAATAGATCACTCGAAAAGATCTGCTTTC 1740  
1806 TCTATTCAGATGAGAAAATCCTTAACCAATAGATCACTCGAAAAGATCTGCTTTC 1859  
1741 AAAACGAAAGCTGAACCTTAAGCAGCAGTATAGCAATATAGCAATCGAATTAATATC 1800  
1860 AAAACGAAAGCTGAACCTTAAGCAGCAGTATAGCAATATAGCAATCGAATTAATATC 1919  
1801 CACAAATCAAGACCTTAAGAAATAGGCTGAGGAGAGTCTTCTACAGGCAATTT 1860  
1920 CACAAATCAAGACCTTAAGAAATAGGCTGAGGAGAGTCTTCTACAGGCAATTT 1979  
1861 CATGCGCTTGAACCTAGTGTAGTCAAGTAAATCTTAAGCCCACTTAATGTTACTGAAATGCAA 1920  
1980 CATGCGCTTGAACCTAGTGTAGTCAAGTAAATCTTAAGCCCACTTAATGTTACTGAAATGCAA 2039  
1921 ATTGATAGTGTCTAGCAGTGAAGAGATAAAGAAAAGATCAACCAATGCCAGTC 1980  
2040 ATTGATAGTGTCTAGCAGTGAAGAGATAAAGAAAAGATCAACCAATGCCAGTC 2099  
1981 AGGCACAGCAAAACCTACACTCATGGAAGTAAAGAACTGCACTGGAGCCCAAGAG 2040  
2106 AGGCACAGCAAAACCTACACTCATGGAAGTAAAGAACTGCACTGGAGCCCAAGAG 2159  
2041 AGTAACCAAGCCAAATGAACACAGCAAGTAAAGAACTGCACTGGAGCCCAAGAG 2100  
2160 AGTAACCAAGCCAAATGAACACAGCAAGTAAAGAACTGCACTGGAGCCCAAGAG 2219  
2101 AAGTTACAAATGACCTGGTCTTTTACTAAGTGTCAAAATACAGTGAATTAAGAA 2160  
2220 AAGTTACAAATGACCTGGTCTTTTACTAAGTGTCAAAATACAGTGAATTAAGAA 2279  
2161 TTTGTCATCTAGCCTTCCAGAGAGAAAAGAGAGAACTAGAAAACAGTTTAAAGTG 2220  
2280 TTTGTCATCTAGCCTTCCAGAGAGAAAAGAGAGAACTAGAAAACAGTTTAAAGTG 2339  
2221 TCTAATTAATGCTGAAGACCCCAAGATCTCATGTTAGTGAAGAAAGGTTTGCAAACT 2280  
2340 TCTAATTAATGCTGAAGACCCCAAGATCTCATGTTAGTGAAGAAAGGTTTGCAAACT 2399  
2281 GAAAGATCTGAGAGAGTAGCAGTATTTCACTGGTACTGGTACTGATTAAGCACTCAG 2340  
2400 GAAAGATCTGAGAGAGTAGCAGTATTTCACTGGTACTGGTACTGATTAAGCACTCAG 2459  
2341 GAAAGATCTGAGTACGGAAGTTAGCACTCTAGGAGAGGCAAAAACAGAACCAATAA 2400  
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2520 TGTGTAGTGTGTCAGGCAATTTGAAAACCCCAAGGCACTAATTCATGTTGTTCCAAA 2579  
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2580 GATAATAGAAATGACACAGAAAGGCTTTAGATATCCATTGGGACATGAAAGTTAACCAAGT 2639  
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3060 CCACCACTTTTCCCACTCAAGTCAATTTGTTTAAACTTAAAGTAAAGAAATCTGCTAGAG 3119  
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Qy 5521 AGTGTAGCACTTACAGTGCAGAGCTGAGACACTTACTGATACCCAGATCCCCAC 5580  
Db 5640 AGTGTAGCACTTACAGTGCAGAGCTGAGACACTTACTGATACCCAGATCCCCAC 5699  
Qy 5581 AGCCACTAC 5589  
Db 5700 AGCCACTAC 5708

RESULT 5  
AAV46468  
ID AAV46468 standard; cDNA; 5711 BP.





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Db 1380 GAATATTTCTGGTTCTTCAGAGAAATAGACTTACTGGCCAGTGTATCTCATGAGGCTTTA 1439  
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QY 4921 GCTTCAACAGAAAGGGTCAACAAAGAAATGTCATGTTGTTGCTGCTGCTGACCCAGAA 4980  
Db 5040 GCTTCAACAGAAAGGGTCAACAAAGAAATGTCATGTTGTTGCTGCTGCTGACCCAGAA 5099  
QY 4981 GAATTTATGCTGTTGTAAGTTTCCAGAAACACCAATCACTTAACTTAACTTAACT 5040  
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Db 5160 ACTGAAGAGACTACTCACTGTTGTTATGAAACAGATGCTGAGTTTGTGTGTGAAACGACA 5219  
QY 5101 CTGAATAATTTCTAGGAATTTGGGAGGAAATGSGTAGTTAGCTTATTTCTGGGTGACC 5160  
Db 5220 CTGAATAATTTCTAGGAATTTGGGAGGAAATGSGTAGTTAGCTTATTTCTGGGTGACC 5279  
QY 5161 CAGTCTATTAAAGAAAGAAATGCTGAATGAGCATGATTTTGAAGTCAAGAGAGATGTG 5220  
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QY 5221 GTCAATGGAAGAAACCAACAGGTCCAAGGAGCAAGAAATCCAGGACAGAAAGATC 5280  
Db 5340 GTCAATGGAAGAAACCAACAGGTCCAAGGAGCAAGAAATCCAGGACAGAAAGATC 5399  
QY 5281 TTCAGGGGCTAGAAATCTGTTGCTATGGCCCTTCCACCAATGCCACAGATCAACTG 5340  
Db 5400 TTCAGGGGCTAGAAATCTGTTGCTATGGCCCTTCCACCAATGCCACAGATCAACTG 5459  
QY 5341 GAATGATGTTACAGCTGTGTGCTTCTGTGTTGAAAGAGGTTTCACTTCACTTCACTT 5400  
Db 5460 GAATGATGTTACAGCTGTGTGCTTCTGTGTTGAAAGAGGTTTCACTTCACTTCACTT 5519  
QY 5401 GGCAAGGTTTCCACCAATTTGTTGTTGCAAGGAGTCCCTGAGCAGAGGAGCAATGGC 5460  
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QY 5461 TTCATGCAATTTGGGAGGATGTTGAGGCACTTGTGTTGCAAGGAGTCCCTGAGGAGTGGGTGGAC 5520  
Db 5580 TTCATGCAATTTGGGAGGATGTTGAGGCACTTGTGTTGCAAGGAGTCCCTGAGGAGTGGGTGGAC 5639  
QY 5521 AGTGTAGCACTTACAGTCCAGAGGAGTCCAGTCTGATGATCCAGATCCGCCAC 5580  
Db 5640 AGTGTAGCACTTACAGTCCAGAGGAGTCCAGTCTGATGATCCGCCAC 5699  
QY 5581 AGCCACTAC 5589

Db 5700 AGCCACTAC 5708  
 RESULT 6  
 AAV46465  
 ID AAV46465 standard; cDNA; 5711 BP.  
 XX AC  
 XX AAV46465;  
 XX  
 DT 18-NOV-1998 (first entry)  
 XX  
 DE Human BRCA1 omi3 polymorphism #1 cDNA.  
 XX  
 KW BRCA1; omi3; human; breast and ovarian cancer predisposing gene;  
 KW polymorphism; susceptibility; anti-oncogene; tumour suppressor;  
 KW chromosome 17q; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 XX Key Location/Qualifiers  
 XX CDS 120..5711  
 XX /tag= a  
 XX /product= "BRCA1 omi3 protein"  
 XX variation 2201  
 XX /tag= b  
 XX /note= "This polymorphic variation can be a C or T  
 XX nucleotide"  
 XX  
 XX US5750400-A.  
 XX  
 XX 12-MAY-1998.  
 XX  
 XX 12-FEB-1997; 97US-00798691.  
 XX  
 XX 12-FEB-1996; 96US-00598591.  
 XX  
 XX (ONCO-) ONCORMED INC.  
 XX  
 XX Olson SJ, Murphy PB, Zeng B, Alvarez CP, Schelter DB, Allen AC;  
 XX Critz BS;  
 XX WPI; 1998-296774/26.  
 XX  
 XX BRCA1 omi gene coding sequences - useful for distinguishing between  
 XX polymorphisms and mutation(s) in the screening for disposition to breast  
 XX or ovarian cancer.  
 XX  
 XX Claim 2e; Page; 54pp; English.  
 XX  
 XX This sequence encodes a human BRCA1 (breast and ovarian cancer  
 XX predisposing gene) omi3 gene in which a polymorphic variation occurs at  
 XX nucleotide 2201. This sequence and other polymorphic variations of this  
 XX sequence are useful for the identification of an individual who may or  
 XX may not have an increased susceptibility to breast or ovarian cancer. The  
 XX sequences used identify gene changes which are due to polymorphisms,  
 XX rather than cancer causing mutations. BRCA1 is an anti-oncogene (tumour  
 XX suppressor) which is involved in genetic inheritance of cancers,  
 XX especially breast and ovarian cancer. It is found at human chromosome 17q  
 XX which is known to be linked to cancer susceptibility, especially breast  
 XX cancer. Cells containing a mutation in this gene lose the wild-type  
 XX function of BRCA1 and are more susceptible to cancers. NOTE: This  
 XX sequence does not appear in the specification but has been created from  
 XX the wild type BRCA1 omi3 gene represented in AAV46450  
 XX  
 XX Sequence 5711 BP; 1953 A; 1098 C; 1277 G; 1382 T; 0 U; 1 Other;  
 XX  
 XX Query Match 100.0%; Score 5588.6; DB 2; Length 5711;  
 XX Best Local Similarity 100.0%; Pred. No. 0;  
 XX Matches 5588; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 XX 1 ATGGATTATCTGCTCTTGGGTTGAAGAGTACAAATGTCATTATATGCTATCGAGAAA 60  
 XX  
 XX 120 ATGGATTATCTGCTCTTGGGTTGAAGAGTACAAATGTCATTATATGCTATCGAGAAA 179

QY 61 ATCTTAGAGTGTCCCATCTGTCTGGAGTTGATCAAGGAACCTGTCTCCCAAGTGTGAC 120  
 Db 180 ATCTTAGAGTGTCCCATCTGTCTGGAGTTGATCAAGGAACCTGTCTCCCAAGTGTGAC 239  
 QY 121 CACATATTTTGCATAATTTTGGCATCTTCAACCAAGAGAGGCTTACAGAG 180  
 Db 240 CACATATTTTGCATAATTTTGGCATCTTCAACCAAGAGAGGCTTACAGAG 239  
 QY 181 TGTCTTTATGTAAGAAATGATATACCAAAAGAGGCTTACAGAGAGGCTTACAG 240  
 Db 300 TGTCTTTATGTAAGAAATGATATACCAAAAGAGGCTTACAGAGAGGCTTACAG 359  
 QY 241 CACATATTTTGCATAATTTTGGCATCTTCAACCAAGAGAGGCTTACAGAG 300  
 Db 360 CACATATTTTGCATAATTTTGGCATCTTCAACCAAGAGAGGCTTACAGAG 419  
 QY 301 TATGCAACAGAGCTATATATTTTGCATAATTTTGGCATCTTCAACCAAGAG 360  
 Db 420 TATGCAACAGAGCTATATATTTTGCATAATTTTGGCATCTTCAACCAAGAG 479  
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 QY 421 GAAACCCGAAATTCCTTCTTGCAGGAAACCCAGTCTCAGTGTCCAACTCTCT 480  
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 QY 481 ACTGTGAGAACTCTGAGGACAAAGCAGGAGTACAACTTCAAGAGAGGCTTGT 540  
 Db 600 ACTGTGAGAACTCTGAGGACAAAGCAGGAGTACAACTTCAAGAGAGGCTTGT 659  
 QY 541 GAATGGGATCTGATTTCTTGAAGATACCGTTAATAAGGCAACTTATTGCA 600  
 Db 660 GAATGGGATCTGATTTCTTGAAGATACCGTTAATAAGGCAACTTATTGCA 719  
 QY 601 GATCAAGAAATGTTTCAAAATCACCCCTCAAGGAAACCCAGGATCAAACTCA 660  
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 QY 661 GCAAAAAGGCTCTGTTGTAATTTCTGAGAGCGATGTAACTCAATCTCAATCA 720  
 Db 780 GCAAAAAGGCTCTGTTGTAATTTCTGAGAGCGATGTAACTCAATCTCAATCA 839  
 QY 721 CCCAGTAATAATGATTTGAAACCACTGAGAAACCGTGCAGCTGAGAGGCA 780  
 Db 840 CCCAGTAATAATGATTTGAAACCACTGAGAAACCGTGCAGCTGAGAGGCA 899  
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 Db 900 TATCAGGTAATGTTCTGTTTCAAACTTGCATGTGGAGCCATGTGCAAAATCT 959  
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 Db 960 AGCTCATTACAGCATGAGAAACAGCAGTTTATTACTCACTAAAGACAGAAAT 1019  
 QY 901 AAGCTGTAATTTGTAATAAAGCAACAGCTGGCTTACAGAGGAGCCACATAC 960  
 Db 1020 AAGCTGTAATTTGTAATAAAGCAACAGCTGGCTTACAGAGGAGCCACATAC 1079  
 QY 961 TGGGCTGGAAGTAAAGAAACATGTAAATGATAGGAGGAGTCCAGACAGAAA 1020  
 Db 1080 TGGGCTGGAAGTAAAGAAACATGTAAATGATAGGAGGAGTCCAGACAGAAA 1139  
 QY 1021 GATCTGAATGCTGATCCCTGTGTGAGAGAAAGAAATGGAATAGCGAGAAAT 1080  
 Db 1140 GATCTGAATGCTGATCCCTGTGTGAGAGAAAGAAATGGAATAGCGAGAAAT 1199  
 QY 1081 TCAGAGAACTCTAGAGTACTGAGAGTGTTCCTTGGATACACTTAATATACAG 1140  
 Db 1200 TCAGAGAACTCTAGAGTACTGAGAGTGTTCCTTGGATACACTTAATATACAG 1259

1141 AAAAGTTAATGAGTGGTTCAGAAAGTGAAGTCACTGTTAGTCTGATGATCTCAATGAT 1200  
1260 AAAAGTTAATGAGTGGTTCAGAAAGTGAAGTCACTGTTAGTCTGATGATCTCAATGAT 1319  
1201 GGGGAGTCTGAATCAAAATGCCAAAGTAGTGTATTTGGACGTTCTAAATGAGGTAGAT 1260  
1320 GGGGAGTCTGAATCAAAATGCCAAAGTAGTGTATTTGGACGTTCTAAATGAGGTAGAT 1379  
1361 GAATATTTCTGTTCTTTCAGAGAAATAGATTAATGAGTGGTCTGATGATCTCAATGAGGTAGAT 1320  
1380 GAATATTTCTGTTCTTTCAGAGAAATAGATTAATGAGTGGTCTGATGATCTCAATGAGGTAGAT 1439  
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1440 ATATGTAAGAGTGAAGAGTTCACCTCAAAATCAGTACAGAGTGAATATTTGAAGACAAATA 1499  
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1560 CTAAATATAGGAGCATTTGTTACTGAGCCACAGATATACAGAGCGTCCCTCACAAT 1619  
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2040 ATTGATAGTGTCTTACAGTGAAGAGATAAAGAAATAAGTACAAACCAATGCCAGTC 2099  
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2160 AGTAACAGGCAATGAACACAGCAAGTAAAGACATGACAGYGTATCTTTCCAGAGCTG 2219  
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2221 TCTAATTAATGCTGAAGACCCCAAGATCTCATGTTAAGTGGAGAAAGGGTTTTCAGAACT 2280

2340 TCTAATTAATGCTGAAGACCCCAAGATCTCATGTTAAGTGGAGAAAGGGTTTTCAGAACT 2399  
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2821 AATGCAAAATGTAGTATCAAGAGGCTCTAGGTTTGTCTATCTCAGTTCAGAGGC 2880  
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3000 AACGAAATCTGAGTCAATTTACCAATAAACATGACATTTTACAAACCCATATCGTATA 3059  
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3180 AGTACAGTGAAGCAATTTAGCCGTAATCAATTTAGAGAAATGTTTTAAAGGAGCCAGC 3239  
3121 TCAAGCAATTTAATGAAGTAGTTTCCAGTACTAATGAAGTGGCTCCAGTATTAATGAA 3180  
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3181 ATAGTTCAGGTGATGAAGCAATTTCAAGCAGAACTAGGTAGAAACAGAGGGCCAAATG 3240  
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3301 AGTAATTTAGCTTCTGAAATTAAGAAACAGAAATATGAAGTGTAGTTCAGACTGTT 3360

Db	3420	AGTAAATTGTGAAGCATCCCTGGAATAATAAAAAAGCAAGAAATATGAGAAAGTAGTTTCAGACACTGTT	3479
Qy	3361	AATACAGAAATTTCTCTCCCATATCTGATTTTCAGATAAATTCAGAACAGCCCTATCGGAAGTAGT	3420
Db	3480	AATACAGAAATTTCTCTCCCATATCTGATTTTCAGATAAATTCAGAACAGCCCTATCGGAAGTAGT	3539
Qy	3421	CATGCATCTCAGGTTTGTTCTGAGACACCTGATGACCTGTTAGATGATGTTGAATTAATTAAG	3480
Db	3540	CATGCATCTCAGGTTTGTTCTGAGACACCTGATGACCTGTTAGATGATGTTGAATTAATTAAG	3599
Qy	3481	GAAGATATCTAGTTTGTCTGAAAAATGACATTAAGGAAAGTCTGCTGTTTTTATAGCAAAAGC	3540
Db	3600	GAAGATATCTAGTTTGTCTGAAAAATGACATTAAGGAAAGTCTGCTGTTTTTATAGCAAAAGC	3659
Qy	3541	GTCCAGAGAGAGACTTTAGCAGGAGTCTTACGCCCTTTCACCCATACACATTTGGCTCAG	3600
Db	3660	GTCCAGAGAGAGAGACTTTAGCAGGAGTCTTACGCCCTTTCACCCATACACATTTGGCTCAG	3719
Qy	3601	GTTTACCAAGCAGGGGCCAAGAAATTAGAGTCTCAGAGAGAGACTTATCTAGTGAGAT	3660
Db	3720	GTTTACCAAGCAGGGGCCAAGAAATTAGAGTCTCAGAGAGAGACTTATCTAGTGAGAT	3779
Qy	3661	GAAGAGCTTCCCTGCTTCCAACTTGTTATTTGGTAAAGTAAACAATATACCTTCTCAG	3720
Db	3780	GAAGAGCTTCCCTGCTTCCAACTTGTTATTTGGTAAAGTAAACAATATACCTTCTCAG	3839
Qy	3721	TCTACTAGGCATAGCACCGTGTCTACCGAGTCTCTGCTTAAGAACACAGAGGAGAAATTTA	3780
Db	3840	TCTACTAGGCATAGCACCGTGTCTACCGAGTCTCTGCTTAAGAACACAGAGGAGAAATTTA	3899
Qy	3781	TTATCATTTGAAGATAGCTTAAATGCACTGCAGTAGTAAACCAAGGTAAATATTTGGCAAAAGGCATCT	3840
Db	3900	TTATCATTTGAAGATAGCTTAAATGCACTGCAGTAGTAAACCAAGGTAAATATTTGGCAAAAGGCATCT	3959
Qy	3841	CAGGAACATCACCTTAGTGAGGAAACAAATTTGTTCTGCTAGCTTGTCTTCTCACAGTGC	3900
Db	3960	CAGGAACATCACCTTAGTGAGGAAACAAATTTGTTCTGCTAGCTTGTCTTCTCACAGTGC	4019
Qy	3901	AGTGAATTGGGAAGACTTGACTGCAAAATACAAACCAACCAAGGATCCCTTTCTTGATTGGTTCT	3960
Db	4020	AGTGAATTGGGAAGACTTGACTGCAAAATACAAACCAACCAAGGATCCCTTTCTTGATTGGTTCT	4079
Qy	3961	TCCAAAACAAATPAGGCATCAGTCTGAAAGCCAGGAGTTGGTCTGAGTGAACAAGAAATTG	4020
Db	4080	TCCAAAACAAATPAGGCATCAGTCTGAAAGCCAGGAGTTGGTCTGAGTGAACAAGAAATTG	4139
Qy	4021	GTTTCAGATGATGAAGAAGAGGAACGGGCTTGGAAAGAAATATCAAGAAGAGCAAGC	4080
Db	4140	GTTTCAGATGATGAAGAAGAGGAACGGGCTTGGAAAGAAATATCAAGAAGAGCAAGC	4199
Qy	4081	ATGGATTCAAACTTAGTGAGCAGCATCTGGGTGTGAGAGTGAGAAACAAGCGTCTCTGAA	4140
Db	4200	ATGGATTCAAACTTAGTGAGCAGCATCTGGGTGTGAGAGTGAGAAACAAGCGTCTCTGAA	4259
Qy	4141	GACTGCTCAGGGCTATCCTCTCAGAGTGACATTTTAAACCACTCAGCAGAGGATACCATG	4200
Db	4260	GACTGCTCAGGGCTATCCTCTCAGAGTGACATTTTAAACCACTCAGCAGAGGATACCATG	4319
Qy	4201	CAACATAACCTGATAAAGCTCCAGCAGGAATGSGCTGAACTAGAAGCTGTGTTAGAACAG	4260
Db	4320	CAACATAACCTGATAAAGCTCCAGCAGGAATGSGCTGAACTAGAAGCTGTGTTAGAACAG	4379
Qy	4261	CATGGAGCCAGCCTTCTTAACAGTACCTTCCATCAATAAGTGACTCTTCTGGCCCTTGAG	4320
Db	4380	CATGGAGCCAGCCTTCTTAACAGTACCTTCCATCAATAAGTGACTCTTCTGGCCCTTGAG	4439
Qy	4321	GACCTGCGAATCCAGAACCAAGCACAATCAGAAAAAGCAGTATTAACTTCCACAGAAAAGT	4380
Db	4440	GACCTGCGAATCCAGAACCAAGCACAATCAGAAAAAGCAGTATTAACTTCCACAGAAAAGT	4499
Qy	4381	AGTGAATCCCTTATAAGCCGAATTCAGAGGCGCTTTCTGCTGACAAAGTTTGAAGTGTCT	4440
Db	4500	AGTGAATCCCTTATAAGCCGAATTCAGAGGCGCTTTCTGCTGACAAAGTTTGAAGTGTCT	4559

QY 5521 AGTGTAGCACTCTACAGTGCAGAGCTGACACCTACCTGATACCCAGATCCCCAC 5580  
 DB 5640 AGTGTAGCACTCTACAGTGCAGAGCTGACACCTACCTGATACCCAGATCCCCAC 5699  
 QY 5591 AGCCACTAC 5589  
 DB 5700 AGCCACTAC 5708

## RESULT 7

ID AAV46470 standard; cDNA; 5711 BP.  
 XX AAV46470;

AC AAV46470;

DT 18-NOV-1998 (first entry)

DE Human BRCA1 omi3 polymorphism #6 cDNA.

XX BRCA1; omi3; human; breast and ovarian cancer predisposing gene;  
 KW polymorphism; susceptibility; anti-oncogene; tumour suppressor;  
 KW chromosome 17q; ss.

XX Homo sapiens.

XX Key Location/Qualifiers  
 XX CD5 120-5711

FT /tag= a  
 FT /product= "BRCA1 omi3 protein"

FT 4427

FT variation

FT /tag= b  
 FT /note= "This polymorphic variation can be a T or C  
 nucleotide"

XX US5750400-A.

XX 12-MAY-1998.

XX 12-FEB-1997; 97US-00798691.

XX 12-FEB-1996; 96US-00598591.

XX (ONCO-) ONCORMED INC.

XX Olson SJ, Murphy PD, Zeng B, Alvares CP, Schelter DB, Allen AC;  
 PI Critz BS;

XX WPI; 1998-296774/26.

XX BRCA1 omi gene coding sequences - useful for distinguishing between  
 PT polymorphisms and mutation(s) in the screening for disposition to breast  
 PT or ovarian cancer.

XX Claim 2e; Page; 54pp; English.

XX This sequence encodes a human BRCA1 (breast and ovarian cancer  
 CC predisposing gene) omi3 gene in which a polymorphic variation occurs at  
 CC nucleotide 4427. This sequence and other polymorphic variations of this  
 CC sequence are useful for the identification of an individual who may or  
 CC may not have an increased susceptibility to breast or ovarian cancer. The  
 CC sequences used identify gene changes which are due to polymorphisms,  
 CC rather than cancer causing mutations. BRCA1 is an anti-oncogene (tumour  
 CC suppressor) which is involved in genetic inheritance of cancers,  
 CC especially breast and ovarian cancer. It is found at human chromosome 17q  
 CC which is known to be linked to cancer susceptibility, especially breast  
 CC cancer. Cells containing a mutation in this gene lose the wild-type  
 CC function of BRCA1 and are more susceptible to cancers. NOTE: This  
 CC sequence does not appear in the specification but has been created from  
 CC the wild type BRCA1 omi3 gene represented in AAV46450

XX Sequence 5711 BP; 1953 A; 1098 C; 1277 G; 1382 T; 0 U; 1 Other;

Query Match

100.0%; Score 5588.6; DB 2; Length 5711;

Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 5588; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ATCGATTATCTGCTCTCTCGCGTTGAGAGGTACAAAATGCTATTATGCTATGTCAGAAA 60  
 DB 120 ATGGAATTAATCTGCTCTCTCGCGTTGAGAGGTACAAAATGCTATTATGCTATGTCAGAAA 179  
 QY 61 ATCTTAGAGTGTCCCATCTGCTGCGAGTTGATCAAGGAACCTGCTCCCAAAAGTGTGAC 120  
 DB 180 ATCTTAGAGTGTCCCATCTGCTGCGAGTTGATCAAGGAACCTGCTCCCAAAAGTGTGAC 239  
 QY 121 CACATATTTTGCATAATTTTGCATGCTGGAACCTTCTCAACGAGAGAAAGGGCCCTTCACAG 180  
 DB 240 CACATATTTTGCATAATTTTGCATGCTGGAACCTTCTCAACGAGAGAAAGGGCCCTTCACAG 299  
 QY 181 TGTCTTTTATGTAAGAAATGATATAACCAAAAGGAGCTTACAGAAAGTACGAGATTAGT 240  
 DB 300 TGTCTTTTATGTAAGAAATGATATAACCAAAAGGAGCTTACAGAAAGTACGAGATTAGT 359  
 QY 241 CAACTTTTGAAGAGCTATTTGAAAATCATTTTGTGCTTTTTCAGCTTGCACACAGTTTGGAG 300  
 DB 360 CAACTTTTGAAGAGCTATTTGAAAATCATTTTGTGCTTTTTCAGCTTGCACACAGTTTGGAG 419  
 QY 301 TATGCAACAGCTATATAATTTTGCAAAAGGAGAAATTAACCTCTCTGAAACATCTTAAAGAT 360  
 DB 420 TATGCAACAGCTATATAATTTTGCAAAAGGAGAAATTAACCTCTCTGAAACATCTTAAAGAT 479  
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 DB 480 GAAGTTTCTATCATCCAAAGTATGGCTACAGAAACCGTGCCCAAAAGACTTCTACAGAGT 539  
 QY 421 GAAACCGGAAATCCCTTCTTGCAGGAAACCAAGTCTCAGTGTCCCACTCTTAACCTTGA 480  
 DB 540 GAAACCGGAAATCCCTTCTTGCAGGAAACCAAGTCTCAGTGTCCCACTCTTAACCTTGA 599  
 QY 481 ACTGTAGAACTCTGAGGACAAAGAGCGGATACAAACCTCAAAAGAGCTTGTCTACATT 540  
 DB 600 ACTGTAGAACTCTGAGGACAAAGAGCGGATACAAACCTCAAAAGAGCTTGTCTACATT 659  
 QY 541 GAATTTGGATCTGATTTCTTCTGAAGATACCGTTTAAAGGCAACTTATTCAGTGTGGA 600  
 DB 660 GAATTTGGATCTGATTTCTTCTGAAGATACCGTTTAAAGGCAACTTATTCAGTGTGGA 719  
 QY 601 GATCAAGAAATGTTTACAAATCAACCTCAAGGAACCAAGGATGAAATCACTGTTGATTCT 660  
 DB 720 GATCAAGAAATGTTTACAAATCAACCTCAAGGAACCAAGGATGAAATCACTGTTGATTCT 779  
 QY 661 GCAAAAAGCGCTTGTGCAATTTTCTGAGAGCGGATGAAATCACTGAACTCATCAA 720  
 DB 780 GCAAAAAGCGCTTGTGCAATTTTCTGAGAGCGGATGAAATCACTGAACTCATCAA 839  
 QY 721 CCAGTAAATGATTTGAACCACTGAGAGCGGATGAGAGGATCCAGAAAAG 780  
 DB 840 CCAGTAAATGATTTGAACCACTGAGAGCGGATGAGAGGATCCAGAAAAG 899  
 QY 781 TATCAGGTAGTCTGTTTCAAACTTGCATGAGAGCGGATGAGGCAAAATCACTCATGCC 840  
 DB 900 TATCAGGTAGTCTGTTTCAAACTTGCATGAGAGCGGATGAGGCAAAATCACTCATGCC 959  
 QY 841 AGCTCAATTACAGCATGAGAACAGCAGTATTACTCACTTAAAGACAGAAATGAATGTAGAA 900  
 DB 960 AGCTCAATTACAGCATGAGAACAGCAGTATTACTCACTTAAAGACAGAAATGAATGTAGAA 1019  
 QY 901 AAGGCTGAATTTCTGTAATAAAGCAAAACAGCTTGGCTTAGCAGAGGAGCCCAATACAGA 960  
 DB 1020 AAGGCTGAATTTCTGTAATAAAGCAAAACAGCCTGGCTTAGCAGAGGAGCCCAATACAGA 1079  
 QY 961 TGGGCTGGAAGTAAGGAAACATGTAATGATAGCGGACTCCACAGCACAGAAAAAGGTA 1020  
 DB 1080 TGGGCTGGAAGTAAGGAAACATGTAATGATAGCGGACTCCACAGCACAGAAAAAGGTA 1139  
 QY 1021 GATCTGAATGCTGATCCCTCTGTTGTAGAGAAAGAAATGGAATGAATAGCAGAAACTGCCATGC 1080



Db 1140 GATCTGAATGCTGATCCCTGCTGTGAGAGAAAGAAATGGAATAGCAAGAACTGCCATGC 1199  
Qy 1081 TCAGAGAACTCTAGAGATCTGAAGATGTTCTCTTGGATAACACATAAATAGCAGCAATTCAG 1140  
Db 1200 TCAGAGAACTCTAGAGATCTGAAGATGTTCTCTTGGATAACACATAAATAGCAGCAATTCAG 1259  
Qy 1141 AAAAGTAAATGAGTGGTCTTTCAGAGAGTGAATGAATGTTAGGTTCTGATGACTCACATGAT 1200  
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Db 1380 GAATATTTCTGCTTCTTCAGAGAAATAGACTTACTGCGCACTGATCTCTCATGAGGCTTTA 1439  
Qy 1321 ATATGTAAAGTGAAGAGTTCAGTCCAAATCAGTAGAGATAATATTGAAGACAAAATA 1380  
Db 1440 ATATGTAAAGTGAAGAGTTCAGTCCAAATCAGTAGAGATAATATTGAAGACAAAATA 1499  
Qy 1381 TTTGGGAAACCTATCGAAGAGCGAAGCCTCCGCACTTAAGCCATGAATCTGAAAT 1440  
Db 1500 TTTGGGAAACCTATCGAAGAGCGAAGCCTCCGCACTTAAGCCATGAATCTGAAAT 1559  
Qy 1441 CTAATATAGAGCAATTTGTTACTGAGCCACAGATAATACAGAGCGTCCCTCACAAAT 1500  
Db 1560 CTAATATAGAGCAATTTGTTACTGAGCCACAGATAATACAGAGCGTCCCTCACAAAT 1619  
Qy 1501 AAATTAAGCGTAAAGAGACCTACATCAGCGCTTCATCTGAGGATTTTATCAAGAAA 1560  
Db 1620 AAATTAAGCGTAAAGAGACCTACATCAGCGCTTCATCTGAGGATTTTATCAAGAAA 1679  
Qy 1561 GCAGATTTGGCAGTTCAAGAGACTCTGAAATGATAAATCAGGGAATCAACCAAGCGAG 1620  
Db 1680 GCAGATTTGGCAGTTCAAGAGACTCTGAAATGATAAATCAGGGAATCAACCAAGCGAG 1739  
Qy 1621 CAGAAATGCTCAAGTGAATATTTAATAATAGTGTCTATGAGATAAATAAAGAGTAT 1680  
Db 1740 CAGAAATGCTCAAGTGAATATTTAATAATAGTGTCTATGAGATAAATAAAGAGTAT 1799  
Qy 1681 TCTATTCAGAAATGAGAAATCTTAACCCATAGAAATCACTCGAAGAAAGATCTGCTTTC 1740  
Db 1800 TCTATTCAGAAATGAGAAATCTTAACCCATAGAAATCACTCGAAGAAAGATCTGCTTTC 1859  
Qy 1741 AAAACGAAAGCTGAACCTATTAAGCAGCAGTATTAAGCAATATGGAATCGAATTAATATC 1800  
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Qy 1801 CACAAATTCAAAGCAGCACTTAAGAGAAATAGGCTGAGGAGGAGTCTTCTACAGGCATATT 1860  
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Db 1980 CATGCGCTTCAAACTAGTAGTCACTAGAAATCTTAAGCCCACTAATTTGTAATGAAATGCAA 2039  
Qy 1921 ATTGATAGTTGTTCTAGCAGTGAAGAGATAAAGAAAAAGTACACCAATATGCCAGTTC 1980  
Db 2040 ATTGATAGTTGTTCTAGCAGTGAAGAGATAAAGAAAAAGTACACCAATATGCCAGTTC 2099  
Qy 1981 AGGCACAGCAGAAACCTTACAACTCATCGAGAGTAAAGAACTCGCACTGAGGCGCAAGAG 2040  
Db 2100 AGGCACAGCAGAAACCTTACAACTCATCGAGAGTAAAGAACTCGCACTGAGGCGCAAGAG 2159  
Qy 2041 AGTAACAGCCAAATGAACAGACAGATTAAGAGACATGACAGTATGATCTTTCCAGAGCTG 2100  
Db 2160 AGTAACAGCCAAATGAACAGACAGATTAAGAGACATGACAGTATGATCTTTCCAGAGCTG 2219  
Qy 2101 AAGTTAAACAAATGCACCTGCTTCTTTACTAAGTGTTCAAATACCAATGAACTTAAGAA 2160  
Db 2220 AAGTTAAACAAATGCACCTGCTTCTTTACTAAGTGTTCAAATACCAATGAACTTAAGAA 2279

Qy 2161 TTTGTCAATCTTAGCTTCCAGAGAGAAAGAAAGAACTAGAAAACAGTTAAAGTG 2220  
Db 2280 TTTGTCAATCTTAGCTTCCAGAGAGAAAGAAAGAACTAGAAAACAGTTAAAGTG 2339  
Qy 2221 TCTAAATAATGCTGAAGACCCCAAGATCTCATGTTAAGTGGAGAAAGGGTTTTGCAAACT 2280  
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Qy 2281 GAAAGATCTGTAGAGTAGAGATTTTCACTGGTACCTGGTACTGATTAATGSCACTCAG 2340  
Db 2400 GAAAGATCTGTAGAGTAGAGATTTTCACTGGTACCTGGTACTGATTAATGSCACTCAG 2459  
Qy 2341 GAAAGTATCTCGTTACTGGAAGTTAGCACTCTAGGGAAGGCAAAACAGAACCAATAAAA 2400  
Db 2460 GAAAGTATCTCGTTACTGGAAGTTAGCACTCTAGGGAAGGCAAAACAGAACCAATAAAA 2519  
Qy 2401 TGTGTGAGTCAGTGTGAGCAATTTGAAAAACCCCAAGGCACTAATTTCAATGTTGTTCCAAA 2460  
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Qy 2461 GATAATAGAAATGACACAGAGGCTTTAAGTATCCATTTGGGACATGAAGTTAACCCAGT 2520  
Db 2580 GATAATAGAAATGACACAGAGGCTTTAAGTATCCATTTGGGACATGAAGTTAACCCAGT 2639  
Qy 2521 CGGGAACCAAGCATAGAAATGGAAGAAAGTGAACCTTGATGCTCAGATATTTGCAGAAATACA 2580  
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Qy 3001 GAAACCTTTGAGGAACATTTCAATGTCACTGAAAGAGAAATGGGAATGAGAACATTTCCA 3060  
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Qy 3181 ATAGTTTCCAGTGTGAACCAATTCAGCAGAACTAGGTAGAAACAGAGGGCCAAATTTG 3240  
Db 3300 ATAGTTTCCAGTGTGAACCAATTCAGCAGAACTAGGTAGAAACAGAGGGCCAAATTTG 3359

QY 3241 AATGCTATGCTTAGATTAGGGTTTGGCAACTGAGGTCTATATAACAAGACTTCTCTGGA 3300  
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QY 3360 AATGCTATGCTTAGATTAGGGTTTGGCAACTGAGGTCTATATAACAAGACTTCTCTGGA 3419  
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DB |||||  
QY 3420 AGTAATCTGAAGCATCTCTGAAATATAAAGCAAGAAATATGAAGTAAGTTCAGACTGTT 3479  
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QY 3361 AATCAGATATCTCTCCATATCTGATTTTCAGATTAACCTTAGAACAGCTTATGGGAAGTAGT 3420  
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QY 3480 AATCAGATATCTCTCCATATCTGATTTTCAGATTAACCTTAGAACAGCTTATGGGAAGTAGT 3539  
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QY 3421 CATGCATCTCAGGTTTGTCTGAGACACCTCATGACCTGTAGATGATGGTGAATAAAG 3480  
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QY 3540 CATGCATCTCAGGTTTGTCTGAGACACCTCATGACCTGTAGATGATGGTGAATAAAG 3599  
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Db 5520 GGCAAGGTGTCCACCAATTGTGTTGTGAGCCAGATGCTTGACAGAGGACAAATGGC 5579  
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 Db 5640 AGGTAGCACTCTACCAAGTCCAGAGCTGGACACCTACTCTGATACCCCGAGATCCCCAC 5699  
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 Db 5700 AGCCACTAC 5708

## RESULT 8

AAV46466

ID AAV46466 standard; cDNA; 5711 BP.

XX

XX

AC AAV46466;

XX 18-NOV-1998 (first entry)

XX Human BRCA1 omi3 polymorphism #2 cDNA.

XX

KW BRCA1; omi3; human; breast and ovarian cancer predisposing gene;

KW polymorphism; susceptibility; anti-oncogene; tumour suppressor;

KW chromosome 17q; ss.

XX

XX Homo sapiens.

XX

XX Key

XX Location/Qualifiers

XX 120..5711

XX /tag= a

XX /product= "BRCA1 omi3 protein"

XX variation

XX 2430

XX /tag= b

XX /note= "This polymorphic variation can be a T or C

XX nucleotide"

XX

XX US5750400-A.

XX

XX 12-MAY-1998.

XX

XX 12-FEB-1997; 97US-00798691.

XX

XX 12-FEB-1996; 96US-00598591.

XX

XX (ONCO-) ONCORMED INC.

XX

XX Olson SJ, Murphy PD, Zeng B, Alvares CP, Schelter DB, Allen AC;

XX Critz BS;

XX WPI; 1998-296774/26.

XX

XX BRCA1 omi gene coding sequences - useful for distinguishing between

XX polymorphisms and mutation(s) in the screening for disposition to breast

XX or ovarian cancer.

XX

XX Claim 2e; Page; 54pp; English.

XX

XX This sequence encodes a human BRCA1 (breast and ovarian cancer

XX predisposing gene) omi3 gene in which a polymorphic variation occurs at

XX nucleotide 2430. This sequence and other polymorphic variations of this

XX sequence are useful for the identification of an individual who may or

XX may not have an increased susceptibility to breast or ovarian cancer. The

XX sequences used identify gene changes which are due to polymorphisms,

XX rather than cancer causing mutations. BRCA1 is an anti-oncogene (tumour

XX suppressor) which is involved in genetic inheritance of cancers,

XX especially breast and ovarian cancer. It is found at human chromosome 17q

XX which is known to be linked to cancer susceptibility, especially breast

XX cancer. Cells containing a mutation in this gene lose the wild-type

XX function of BRCA1 and are more susceptible to cancers. NOTE: This

XX

XX

XX

XX

XX

XX

XX

XX

XX

CC sequence does not appear in the specification but has been created from  
 CC the wild type BRCA1 omi3 gene represented in AAV46450  
 XX  
 SQ Sequence 5711 BP; 1953 A; 1097 C; 1277 G; 1383 T; 0 U; 1 Other;  
 Query Match 100.0%; Score 5588.6; DB 2; Length 5711;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 5588; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 ATCGATTATATCTCTCTTGGCGTTGAGAGAGTACAAAATGTCTAATATGCTATGTCAGAAA 60  
 Db 120 ATGGAATTATCTGCTCTTGGCGTTGAGAGAGTACAAAATGTCTAATATGCTATGTCAGAAA 179  
 Qy 61 ATCTTAGAGTGTCCCATCTCTCTGGAGTTGATCAAGGAACCTGTCTCCCAAAAGTGTGAC 120  
 Db 180 ATCTTAGAGTGTCCCATCTCTCTGGAGTTGATCAAGGAACCTGTCTCCCAAAAGTGTGAC 239  
 Qy 121 CACATATTTTGCATAATTTTGCATGCTGAAACTTCTCAACGAGAGAAAGGGCTTCCACAG 180  
 Db 240 CACATATTTTGCATAATTTTGCATGCTGAAACTTCTCAACGAGAGAAAGGGCTTCCACAG 299  
 Qy 181 TGTCTTTATGTAAAGATGATATATACCAAAAGAGGCTTACAGAAAGTACGAGATTTAGT 240  
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 Qy 241 CAACTTTTTCAGAGCTATTTGAAATCAATTTGCTTTTCAGCTTTCACACAGGTTGGAG 300  
 Db 360 CAACTTTTTCAGAGCTATTTGAAATCAATTTGCTTTTCAGCTTTCACACAGGTTGGAG 419  
 Qy 301 TATGCAAAACAGCTATATAATTTTGCAAAAGAGGAAATAAATCTCTCTGAAACATCTAAAGAT 360  
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 Db 660 GAATTGGGATCTGATTTCTTGAAGATACCGTTTAATAAGCAACTTATTGCACTGTGGGA 719  
 Qy 601 GATCAAGAAATTTGTACAAATCACCCCTCAAGGAACCCAGGGATGAAATCAGTTTGGATTCT 660  
 Db 720 GATCAAGAAATTTGTACAAATCACCCCTCAAGGAACCCAGGGATGAAATCAGTTTGGATTCT 779  
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 Db 780 GCAAAAGGCTGCTTGTGAAATTTCTGAGAGCGGATGTAACAAATCTGAATCATCAAA 839  
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 Db 840 CCAGTAATAATGATTGAAACACCACTGAGAAACCGTGCAGCTGAGAGGATCCAGAAAAG 899  
 Qy 781 TATCAGGGTAGTCTCTTTTCAAACTTGTGATGTGGAGCCATGTGGCAAAATCTCATGCC 840  
 Db 900 TATCAGGGTAGTCTCTTTTCAAACTTGTGATGTGGAGCCATGTGGCAAAATCTCATGCC 959  
 Qy 841 AGTCTAATCAGCATCAGAAACAGCAGTTTATTACTCCTTAAAGACAGAAATGAATGTAGAA 900  
 Db 960 AGTCTAATCAGCATCAGAAACAGCAGTTTATTACTCCTTAAAGACAGAAATGAATGTAGAA 1019  
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 Db 1020 AAGGCTGAATTTCTGTAATAAAGCAAAACAGCTGGCTTTAGCAAGGACCAACATAACAGA 1079



3240 TCAAGCAATTAATAAGTAGTGTTCAGTACTAATGAAGTGGCTCCAGTATTAATGA 3299 Db  
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 QY 5580 TTCCATGCAATTTGGCAGATGCTGAGGCACTGTGTGACCCGAGTGGTCTTGGAC 5639  
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 QY 5700 AGCCACTAC 5708

RESULT 9  
 AAV46467  
 ID AAV46467 standard; cDNA; 5711 BP.  
 XX  
 AC AAV46467;  
 XX  
 DT 18-NOV-1998 (first entry)  
 XX  
 DE Human BRCA1 omi3 polymorphism #3 cDNA.  
 XX  
 KW BRCA1; omi3; human; breast and ovarian cancer predisposing gene;  
 KW polymorphism; susceptibility; anti-oncogene; tumour suppressor;  
 KW chromosome 17q; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 120..5711  
 FT /\*tag= a  
 FT /product= "BRCA1 omi3 protein"  
 FT 2731  
 FT variation /\*tag= b  
 FT /note= "This polymorphic variation can be a C or T  
 FT nucleotide"  
 XX  
 PN US5750400-A.  
 XX  
 PD 12-MAY-1998.  
 XX  
 PP 12-FEB-1997; 97US-00798691. —  
 XX  
 PR 12-FEB-1996; 96US-00598591. —  
 XX  
 PA (ONCO-) ONCORMED INC.  
 XX  
 PI Olson SJ, Murphy PD, Zeng B, Alvares CP, Schelter DB, Allen AC;  
 PI Critz BS;  
 XX  
 WI; 1998-296774/26.  
 XX

BRCA1 omi gene coding sequences - useful for distinguishing between  
 polymorphisms and mutation(s) in the screening for disposition to breast  
 or ovarian cancer.  
 Claim 2e; Page; 54pp; English.  
 This sequence encodes a human BRCA1 (breast and ovarian cancer  
 predisposing gene) omi3 gene in which a polymorphic variation occurs at  
 nucleotide 2731. This sequence and other polymorphic variations of this  
 sequence are useful for the identification of an individual who may or  
 may not have an increased susceptibility to breast or ovarian cancer. The  
 sequences used identify gene changes which are due to polymorphisms,

CC rather than cancer causing mutations. BRCA1 is an anti-oncogene (tumour  
 suppressor) which is involved in genetic inheritance of cancers,  
 CC especially breast and ovarian cancer. It is found at human chromosome 17q  
 CC which is known to be linked to cancer susceptibility, especially breast  
 CC cancer. Cells containing a mutation in this gene lose the wild-type  
 CC function of BRCA1 and are more susceptible to cancers. NOTE: This  
 CC sequence does not appear in the specification but has been created from  
 CC the wild type BRCA1 omi3 gene represented in AAV46450  
 XX  
 SQ Sequence 5711 BP; 1953 A; 1098 C; 1277 G; 1382 T; 0 U; 1 Other;  
 Query Match 100.0%; Score 5588.6; DB 2; Length 5711;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 5588; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ATCGATTATCTGCTCTCTCGCTTGAAGAGTACAAAATGTCTAATATGCTATGCGAGAA 60  
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 QY 120 ATGGAATTTATCTGCTCTCTCGCTTGAAGAGTACAAAATGTCTAATATGCTATGCGAGAA 179  
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 QY 180 ATCTTAGAGTGTCCTCATCTGTCTGGAGTTGATCAAGAAACCTGTCTCCCAAAAGTGTGAC 239  
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 QY 240 CACATATTTTGCAAATTTTGCATGCTGAAACTTCTCAACGAGAGAAAGGCGCTTCACAG 299  
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 QY 900 TATCAGGAGTGTCTGTTTCAAACTTGCATGTGGAGCCATGTGGCACAATCTCATGCC 959  
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 QY 841 ACCTCATTTACGATGAGAAACAGAGCTTTATTTACTTCACTTAAGAGACAGATGAATGAGAA 900  
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960 AGCTCATTTACAGCATGAGACAGCAGTTTATTACTACTAAGACAGAAATGAATGACAA 1019  
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QY 3541 GTCCAGAGAGAGAGCTTAGCAGAGTCTTAGGCCCTTTACCCATACACATTTGCTCAG 3600  
DB 3660 GTCCAGAGAGAGAGCTTAGCAGAGTCTTAGGCCCTTTACCCATACACATTTGCTCAG 3719  
QY 3601 GGTACCGAAGAGGGGCCAAGAAATAGAGTCTCAGAGAGAACTTATCTAGTGAAGAT 3660  
DB 3720 GGTACCGAAGAGGGGCCAAGAAATAGAGTCTCAGAGAGAACTTATCTAGTGAAGAT 3779  
QY 3661 GAAGGCTTCCTGCTCCACACTGTTATTTGTTAAAGTAAACATATACCTTCTCAG 3720  
DB 3780 GAAGGCTTCCTGCTCCACACTGTTATTTGTTAAAGTAAACATATACCTTCTCAG 3839  
QY 3721 TCTACTAGGCATAGCACGGTTGCTACCGAGTGTCTGCTTAAGAACACAGAGAGAAATTA 3780  
DB 3840 TCTACTAGGCATAGCACGGTTGCTACCGAGTGTCTGCTTAAGAACACAGAGAGAAATTA 3899  
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DB 3900 TTATCATTTGAAGATAGCTTAATGAGTCAAGTAAACAGGTAAATTTGGCAAGGATCT 3959  
QY 3841 CAGGAAATACACCTTAGTGAGGAAACAAATGTTCTGCTAGCTGTTTTCTTCACAGTGC 3900  
DB 3960 CAGGAAATACACCTTAGTGAGGAAACAAATGTTCTGCTAGCTGTTTTCTTCACAGTGC 4019  
QY 3901 AGTGATTTGGAAGACTTGACTGCAAAATACAAACACCGAGGATCTTTCTGATTTGTTCT 3960  
DB 4020 AGTGATTTGGAAGACTTGACTGCAAAATACAAACACCGAGGATCTTTCTGATTTGTTCT 4079  
QY 3961 TCCAAACAAATGAGGCAATCAGTCTGAAAGCCAGGAGTTGGTCTGAGTGCAGAGAAATG 4020  
DB 4080 TCCAAACAAATGAGGCAATCAGTCTGAAAGCCAGGAGTTGGTCTGAGTGCAGAGAAATG 4139  
QY 4021 GTTTTCAGATGATGAAGAAAGAGAACCGGCTTGAAGAAATATCAAGAGAGCAAGC 4080  
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DB 4200 ATGGATTCAAACTTAGGTGAGAGAGCATCTGGGTGAGAGTGAACCAAGGCTCTGAA 4259  
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QY 4321 GACTGGGAATCCAGAACCAAGACCATCAGAAAGACAGTATTAATCTCAGAAAGT 4380  
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QY 4441 GCAGATAGTTCTACCGATTAATAAAGAAACAGAGAGTGGAAAGGTCACTCCCTTCTAAA 4500  
DB 4560 GCAGATAGTTCTACCGATTAATAAAGAAACAGAGAGTGGAAAGGTCACTCCCTTCTAAA 4619  
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DB 4620 TGCCCATCATTTAGATGATAGTGTGTACATGACAGTTGCTCTGGAGTCTTCAGATAGA 4679  
QY 4561 AACTACCCATCTCAAGAGGAGTCTAATAAGTTGTTGATGTGGAGAGCAACAGCTGGAA 4620  
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DB 5040 GCTTCAACAGAAAGGTTCAACAAAGAAATGTCATGCTGTTGCTGGCTGACCCAGAA 5099  
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DB 5280 CAGTCTTTAAAGAAAGAAATGCTGATGAGCATGATTTTCAAGTCAAGAGGATGTTG 5339  
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Db 5340 GTCAATGGAGAAACCCACCAAGGTCCTCAAGCGAGCAAGAGATCCAGGACAGAAAGATC 5399  
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Db 5400 TTCAGGGGCTAGAAATCTGTGCTATGGGCGCTTCAACCAATGCCACAGATCAATCG 5459  
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Db 5640 AGTGTAGCACTTACAGTGCAGGAGCTGTGACACCTTACCTGATACCCGAGATCCCCAC 5699  
QY 5581 AGCCACTAC 5589  
Db 5700 AGCCACTAC 5708

RESULT 10  
AAV46469  
ID AAV46469 standard; cDNA; 5711 BP.  
AC AAV46469;  
XX  
XX  
DT 18-NOV-1998 (first entry)  
XX  
DE Human BRCA1 omi3 polymorphism #5 cDNA.  
XX  
KW BRCA1; omi2; human; breast and ovarian cancer predisposing gene;  
KW polymorphism; susceptibility; anti-oncogene; tumour suppressor;  
KW chromosome 17q; ss.  
XX  
OS Homo sapiens.  
XX  
XX  
FH Key Location/Qualifiers  
FT CDS 120..5711  
FT /\*tag= a  
FT /product= "BRCA1 omi3 protein"  
FT variation 3667  
FT /\*tag= b  
FT /note= "This polymorphic variation can be an A or G  
XX nucleotide"  
PN US5750400-A.  
XX  
XX PD 12-MAY-1998.  
XX  
XX PP 12-FEB-1997; 97US-00798691.  
XX  
XX PR 12-FEB-1996; 96US-00598591 ✓  
XX  
XX PA (ONCO-) ONCORMED INC.  
XX  
XX Olson SJ, Murphy PD, Zeng B, Alvares CP, Scheiter DB, Allen AC;  
XX Critz BS;  
XX  
XX WPI; 1998-296774/26.  
XX  
XX BRCA1 omi gene coding sequences - useful for distinguishing between  
XX polymorphisms and mutation(s) in the screening for disposition to breast  
XX or ovarian cancer.  
XX  
XX PS Claim 2e; Page; 54pp; English.  
XX

CC This sequence encodes a human BRCA1 (breast and ovarian cancer  
CC predisposing gene) omi3 gene in which a polymorphic variation occurs at  
CC nucleotide 3667. This sequence and other polymorphic variations of this  
CC sequence are useful for the identification of an individual who may or  
CC may not have an increased susceptibility to breast or ovarian cancer. The  
CC sequences used identify gene changes which are due to polymorphisms,  
CC rather than cancer causing mutations. BRCA1 is an anti-oncogene (tumour  
CC suppressor) which is involved in genetic inheritance of cancers,  
CC especially breast and ovarian cancer. It is found at human chromosome 17q  
CC which is known to be linked to cancer susceptibility, especially breast  
CC cancer. Cells containing a mutation in this gene lose the wild-type  
CC function of BRCA1 and are more susceptible to cancers. NOTE: This  
CC sequence does not appear in the specification but has been created from  
CC the wild type BRCA1 omi3 gene represented in AAV46450  
XX  
XX Sequence 5711 BP; 1953 A; 1098 C; 1276 G; 1383 T; 0 U; 1 Other;  
SQ  
  
Query Match 100.0%; Score 5588.6; DB 2; Length 5711;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 5588; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 ATGGATTTATCTGCTCTTCGGTTGAAGAGTCAAAATGTCATTATGCTATGCAGAAA 60  
Db 120 ATGGATTTATCTGCTCTTCGGTTGAAGAGTCAAAATGTCATTATGCTATGCAGAAA 179  
QY 61 ATCTTAGAGTGTCCCATCTGTCTGGAGTTCATCAAGGAACTGTCTCCCAAAAGTGTGAC 120  
Db 180 ATCTTAGAGTGTCCCATCTGTCTGGAGTTCATCAAGGAACTGTCTCCCAAAAGTGTGAC 239  
QY 121 CACATATTTGCAAAATTTGCTGCTGAAACTTCTCAACGAGAGAAAGGCGCTTCACAG 180  
Db 240 CACATATTTGCAAAATTTGCTGCTGAAACTTCTCAACGAGAGAAAGGCGCTTCACAG 299  
QY 181 TGTCTTTATGTAAAGATGATATAACCAAGAGAGCTTCAAGAAAGTACGAGATTTAGT 240  
Db 300 TGTCTTTATGTAAAGATGATATAACCAAGAGAGCTTCAAGAAAGTACGAGATTTAGT 359  
QY 241 CAATCTTGTGAAGAGCTATTTGAAAATCAATTTGCTTTTTCAGTTGACAGGTTTCGAG 300  
Db 360 CAATCTTGTGAAGAGCTATTTGAAAATCAATTTGCTTTTTCAGTTGACAGGTTTCGAG 419  
QY 301 TATGCAAAAGCTATTAATTTTGCAAAAAGAGAAATAAATCTCTCTGAACATCTTAAAGAT 360  
Db 420 TATGCAAAAGCTATTAATTTTGCAAAAAGAGAAATAAATCTCTCTGAACATCTTAAAGAT 479  
QY 361 GAAATTTCTATCATCCAAAGTATGGGCTACAGAAACCGTCCCAAAAGACTTCTACAGAGT 420  
Db 480 GAAATTTCTATCATCCAAAGTATGGGCTACAGAAACCGTCCCAAAAGACTTCTACAGAGT 539  
QY 421 GAACCCGAAATCTCTCTTTCGAGGAAACCAAGTCTCAGTGTCCCAACTCTTACCTTGA 480  
Db 540 GAACCCGAAATCTCTCTTTCGAGGAAACCAAGTCTCAGTGTCCCAACTCTTACCTTGA 599  
QY 481 ACTGTGAGAACTCTGAGGCAAAAGCGGATACAACCTCAAAGAGCGTCTGTCTACATT 540  
Db 600 ACTGTGAGAACTCTGAGGCAAAAGCGGATACAACCTCAAAGAGCGTCTGTCTACATT 659  
QY 541 GAAATGGGATCTGATTTCTTCTGAAGATACCGTTAATAAGCAACTTATTCAGTGTGGGA 600  
Db 660 GAAATGGGATCTGATTTCTTCTGAAGATACCGTTAATAAGCAACTTATTCAGTGTGGGA 719  
QY 601 GATCAAGAAATTTGTTACAAATCAACCTCAAGGAAACGAGGATCAAAATCAGTTTGAATCT 660  
Db 720 GATCAAGAAATTTGTTACAAATCAACCTCAAGGAAACGAGGATCAAAATCAGTTTGAATCT 779  
QY 661 GCAAAAAGGCTGCTGTGAAATTTTCTGAGAAGGATGTAAACAAATCTGAACATCATCAA 720  
Db 780 GCAAAAAGGCTGCTGTGAAATTTTCTGAGAAGGATGTAAACAAATCTGAACATCATCAA 839  
QY 721 CCGAGTAATAATGATTTGACCACTCTGAGAGCGGTGACGCTGAGAGGATCCAGAAAG 780  
Db 840 CCGAGTAATAATGATTTGACCACTCTGAGAGCGGTGACGCTGAGAGGATCCAGAAAG 899

QY 781 TATCAGGCTAGTCTCTGTTTCAAACTTGCATGTGGAGCCATGTGGCACAATACTCATGCC 840  
Db 900 TATCAGGCTAGTCTCTGTTTCAAACTTGCATGTGGAGCCATGTGGCACAATACTCATGCC 959  
QY 841 AGCTCATTACAGCATGAGCAACAGCAGTCTTATTACTCACTTAAAGCAGCAATCAATGTAGAA 900  
Db 960 AGCTCATTACAGCATGAGCAACAGCAGTCTTATTACTCACTTAAAGCAGCAATCAATGTAGAA 1019  
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Db 1020 AAGGCTGAATCTGTATAAAGCAACAGCCTGCTTACAGAGGCAACATTAACAGA 1079  
QY 961 TGGGCTGGAAGTAAAGCAACATGTAAATGATAGGCGGACTCCAGCACAAGAAAAAGGTA 1020  
Db 1080 TGGGCTGGAAGTAAAGCAACATGTAAATGATAGGCGGACTCCAGCACAAGAAAAAGGTA 1139  
QY 1021 GATCTGAATCTGTATCCCTGTGTGAGAGAAAAAGAAATGGAATAGCAAACTGCCATGC 1080  
Db 1140 GATCTGAATCTGTATCCCTGTGTGAGAGAAAAAGAAATGGAATAGCAAACTGCCATGC 1199  
QY 1081 TCAGAGATCCTAGAGATCTGAAGATCTCTCTGATAGCAACATTAATAGCAGCATTCAG 1140  
Db 1200 TCAGAGATCCTAGAGATCTGAAGATCTCTCTGATAGCAACATTAATAGCAGCATTCAG 1259  
QY 1141 AAAGTTAATAGTGGTTTTCCAGAGATGATGAACCTGTGTAGTCTCATCATGAT 1200  
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QY 1561 GCAGATTTGGCAGTTCAAAAGACTCCTGAAATGATAAATCAGGGAATTAACCAACGGAG 1620  
Db 1680 GCAGATTTGGCAGTTCAAAAGACTCCTGAAATGATAAATCAGGGAATTAACCAACGGAG 1739  
QY 1621 CAGATGCTCAAGTGAATGATTAATTAATAGTGGTCAATGAGATTAACCAAGGTTGAT 1680  
Db 1740 CAGATGCTCAAGTGAATGATTAATTAATAGTGGTCAATGAGATTAACCAAGGTTGAT 1799  
QY 1681 TCTATTCAAGATGAGAAAAATCCTAAACCAATAGAACTCACTCGAAAAAGAAATCTGCTTTC 1740  
Db 1800 TCTATTCAAGATGAGAAAAATCCTAAACCAATAGAACTCACTCGAAAAAGAAATCTGCTTTC 1859  
QY 1741 AAAACGAAGCTGAACCTTAAGCAGCGATATAGCAATATGGAACCTGAATTAATATC 1800  
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QY 1801 CACAATTCAAAGCACTTAAAAAGAAATAGGCTGAGGAGGAGTCTTCTTACGAGCATATT 1860  
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QY 2521 CGGAAAACAGCATAGAAATGGAAGAGTGAACCTTGATGCTCAGTATTTGCAAGATACA 2580  
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QY 2941 CCACCACTTTTCCCAATCAAGTCAATTTGTTTAAACCTAATGTAAGAAAAATCTGCTAGAG 3000

Db 3060 CCACCACCTTTTCCCATCAAGTCATTTGTTAAACCTAAATGTAAGAAAAATCTCTAGAG 3119  
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Db 3960 CAGGAACATCACCTTTAGTGAGGAACAAATGTTCTGCTAGCTTGTGTTTCTTCCAGTGC 4019  
Qy 3901 AGTGAATTTGAAGACTTGACTGCAATATCAAAACCCAGGATCCTTTCTTGAATGTTCT 3960  
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Qy 3961 TCCAAACAAATGAGGCTCAGTCTGAAGCCAGGAGTGGCTGAGTGACAGGATTTG 4020  
Db 4080 TCCAAACAAATGAGGCTCAGTCTGAAGCCAGGAGTGGCTGAGTGACAGGATTTG 4139  
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Db 4260 GACTGTCTCAGGGCTATCTCTCTCAGAGTGACATTTTAAACCACTCAGCAGAGGGATACCATG 4319  
Qy 4201 CAACATAACCTGATATAAGCTCCAGAGGAATGGCTGAACTAGAACTGTGTGTAGAACAG 4260  
Db 4320 CAACATAACCTGATATAAGCTCCAGAGGAATGGCTGAACTAGAACTGTGTGTAGAACAG 4379  
Qy 4261 CATGGAGCCAGCCTTTCTAACAGCTACCTTCCATCATTAAGTCACTCTTCTGCCCCTTGAG 4320  
Db 4380 CATGGAGCCAGCCTTTCTAACAGCTACCTTCCATCATTAAGTCACTCTTCTGCCCCTTGAG 4439  
Qy 4321 GACTCTGGAAATCCAGAACAAAGCAATCCAGAAAGCAGTATTAACCTCAGAGAAAGT 4380  
Db 4440 GACTCTGGAAATCCAGAACAAAGCAATCCAGAAAGCAGTATTAACCTCAGAGAAAGT 4499  
Qy 4381 AGTGAATACCTTATAGCCAGGAATCCAGAGGCTTTTCTGCTGACAAAGTTTGAAGTGTCT 4440  
Db 4500 AGTGAATACCTTATAGCCAGGAATCCAGAGGCTTTTCTGCTGACAAAGTTTGAAGTGTCT 4559  
Qy 4441 GCAGATAGTTCTACCAAGTAAATAAAGAACCAAGAGTGAAGAGTCACTCCCTTCTTAA 4500  
Db 4560 GCAGATAGTTCTACCAAGTAAATAAAGAACCAAGAGTGAAGAGTCACTCCCTTCTTAA 4619  
Qy 4501 TGCCCATCATTAAGTATAGGTGATCATGACAGTTGCTCTGGAGTCTTTCAGAAATAGA 4560  
Db 4620 TGCCCATCATTAAGTATAGGTGATCATGACAGTTGCTCTGGAGTCTTTCAGAAATAGA 4679  
Qy 4561 AACTACCCATCTCAAGAGAGCTCATTAAGTTTGTATGTGGAGGAGCAACAGCTGGAA 4620  
Db 4680 AACTACCCATCTCAAGAGAGCTCATTAAGTTTGTATGTGGAGGAGCAACAGCTGGAA 4739  
Qy 4621 GAGCTGTGGGCCACACCATTTGAGGAACATCTTACTGCCAGGCAAGATCTAGAGGGA 4680  
Db 4740 GAGCTGTGGGCCACACCATTTGAGGAACATCTTACTGCCAGGCAAGATCTAGAGGGA 4799  
Qy 4681 ACCCTTACCTGGAATCTGGAATCAGCCTCTTCTCTGATGACCCCTGAATCTGATCTCTCT 4740  
Db 4800 ACCCTTACCTGGAATCTGGAATCAGCCTCTTCTCTGATGACCCCTGAATCTGATCTCTCT 4859  
Qy 4741 GAAGACAGAGCCCGCAGAGTCACTCGTGTGGCAACATACCATCTTCAACCTCTGCAATG 4800  
Db 4860 GAAGACAGAGCCCGCAGAGTCACTCGTGTGGCAACATACCATCTTCAACCTCTGCAATG 4919  
Qy 4801 AAAGTTCCCAATTTGAAGTTGCAAGTCTGCCAGGCTCCAGCTGCTGCTCATACTACT 4860  
Db 4920 AAAGTTCCCAATTTGAAGTTGCAAGTCTGCCAGGCTCCAGCTGCTGCTCATACTACT 4979  
Qy 4861 GATACTGTGGGTATTAATGCAATGGAAGAAAGTGTGAGCAGGGAGGAAGCAGAAATTTGACA 4920  
Db 4980 GATACTGTGGGTATTAATGCAATGGAAGAAAGTGTGAGCAGGGAGGAAGCAGAAATTTGACA 5039  
Qy 4921 GCTTCAACAGAAAGGCTCAACAAAGAAATGTCATGCTGCTGTCTGCGCTGAGCCCGAGAA 4980  
Db 5040 GCTTCAACAGAAAGGCTCAACAAAGAAATGTCATGCTGCTGTCTGCGCTGAGCCCGAGAA 5099  
Qy 4981 GAAATTTATGCTCGTGTACAAAGTTTGCCAGAAACCAACATCACTTTAACTAATCTAAAT 5040  
Db 5100 GAAATTTATGCTCGTGTACAAAGTTTGCCAGAAACCAACATCACTTTAACTAATCTAAAT 5159  
Qy 5041 ACTGAGAGACTACTCATCTGTTATGAAGAAAGTGTGAGTGTGTGTGTAAGGACA 5100  
Db 5160 ACTGAGAGACTACTCATCTGTTATGAAGAAAGTGTGAGTGTGTGTGTAAGGACA 5219  
Qy 5101 CTGAAATATTTTCTAGGAATTCGGGAGGAAGTGGTATGTAGCTATTTCTGGGTGACC 5160  
Db 5220 CTGAAATATTTTCTAGGAATTCGGGAGGAAGTGGTATGTAGCTATTTCTGGGTGACC 5279

QY 5161 CAGTCTATTAAAGAAAGAAATGCTGAATGAGCATGATTTTGAAGTCAGAGGAGATGTG 5220  
 DB |||||  
 QY 5280 CAGTCTATTAAAGAAAGAAATGCTGAATGAGCATGATTTTGAAGTCAGAGGAGATGTG 5339  
 DB |||||  
 QY 5221 GTCAATGGAAGAAACCAACAGAGTCCAAAGCGAGCAAGAGATCCAGGACAGAAAGATC 5280  
 DB |||||  
 QY 5340 GTCAATGGAAGAAACCAACAGAGTCCAAAGCGAGCAAGAGATCCAGGACAGAAAGATC 5399  
 DB |||||  
 QY 5281 TTCAAGGGGCTAGAAATCTGTTGCTATGAGGCTCTTCAACACATGCCACAGATCAACTG 5340  
 DB |||||  
 QY 5400 TTCAAGGGGCTAGAAATCTGTTGCTATGAGGCTCTTCAACACATGCCACAGATCAACTG 5459  
 DB |||||  
 QY 5341 GAATGATGATACAGCTGTGCTGCTCTGTTGTTGAAGAGCTTTTCATCATTTCAACCTT 5400  
 DB |||||  
 QY 5460 GAATGATGATACAGCTGTGCTGCTCTGTTGTTGAAGAGCTTTTCATCATTTCAACCTT 5519  
 DB |||||  
 QY 5401 GGCACAGGTGTCACCAATTTGTTGTTGTCAGCCAGATGCTGACAGAGAGCAATGGC 5460  
 DB |||||  
 QY 5520 GGCACAGGTGTCACCAATTTGTTGTTGTCAGCCAGATGCTGACAGAGAGCAATGGC 5579  
 DB |||||  
 QY 5461 TTCCATGCAATTTGGGCGAGATGTCAGAGCACTGTGTTGACCCGAGAGTGGTGTGGAC 5520  
 DB |||||  
 QY 5580 TTCCATGCAATTTGGGCGAGATGTCAGAGCACTGTGTTGACCCGAGAGTGGTGTGGAC 5639  
 DB |||||  
 QY 5521 AGTGATGACACTACCACTGTCAGAGCTGACACCTACCTGATACCCAGATCCCCAC 5580  
 DB |||||  
 QY 5640 AGTGATGACACTACCACTGTCAGAGCTGACACCTACCTGATACCCAGATCCCCAC 5699  
 DB |||||  
 QY 5581 AGCCACTAC 5589  
 DB |||||  
 QY 5700 AGCCACTAC 5708  
 DB |||||

RESULT 11  
 AAV46456  
 ID AAV46456 standard; cDNA; 5711 BP.  
 AC AAV46456;  
 XX |||||  
 XX |||||  
 DT 18-NOV-1998 (first entry)  
 XX |||||  
 DE Human BRCA1 omil polymorphism #6 cDNA.  
 XX |||||  
 KW BRCA1; omil; human; breast and ovarian cancer predisposing gene;  
 KW polymorphism; susceptibility; anti-oncogene; tumour suppressor;  
 KW chromosome 17q; ss.  
 XX |||||  
 OS Homo sapiens.  
 XX |||||  
 FH Location/Qualifiers  
 FT CDS 120..5711  
 FT |||||  
 FT /\*tag= a  
 FT /product= "BRCA1 omil protein"  
 FT variation 4427  
 FT /\*tag= b  
 FT /note= "This polymorphic variation can be a T or C nucleotide"  
 FT |||||  
 FN US5750400-A.  
 XX |||||  
 PD 12-MAY-1998.  
 XX |||||  
 PP 12-FEB-1997; 97US-00798691.  
 XX |||||  
 PR 12-FEB-1996; 96US-00598591.  
 XX |||||  
 PA (ONCO-) ONCORMED INC.  
 XX |||||  
 PI Olson SJ, Murphy PD, Zeng B, Alvares CP, Schelter DB, Allen AC;  
 PI Critz BS;  
 XX |||||  
 DR WPI; 1998-296774/26.  
 XX |||||

PT BRCA1 omi gene coding sequences - useful for distinguishing between  
 PT polymorphisms and mutation(s) in the screening for disposition to breast  
 PT or ovarian cancer.  
 XX Claim 2e; Page; 54pp; English.  
 XX |||||  
 CC This sequence encodes a human BRCA1 (breast and ovarian cancer  
 CC predisposing gene) omil gene in which a polymorphic variation occurs at  
 CC nucleotide 4427. This sequence and other polymorphic variations of this  
 CC sequence are useful for the identification of an individual who may or  
 CC may not have an increased susceptibility to breast or ovarian cancer. The  
 CC sequences used identify gene changes which are due to polymorphisms,  
 CC rather than cancer causing mutations. BRCA1 is an anti-oncogene (tumour  
 CC suppressor) which is involved in genetic inheritance of cancers,  
 CC especially breast and ovarian cancer. It is found at human chromosome 17q  
 CC which is known to be linked to cancer susceptibility, especially breast  
 CC cancer. Cells containing a mutation in this gene lose the wild-type  
 CC function of BRCA1 and are more susceptible to cancers. NOTE: This  
 CC sequence does not appear in the specification but has been created from  
 CC the wild type BRCA1 omil gene represented in AAV46448  
 XX |||||  
 SQ Sequence 5711 BP; 1953 A; 1098 C; 1277 G; 1382 T; 0 U; 1 Other;  
 |||||  
 Query Match 100.0%; Score 5588.6; DB 2; Length 5711;  
 Best Local Similarity 100.0%; Pred No 0;  
 Matches 5588; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 |||||

QY 1 ATGATTTATCTCTCTTCGCGTTGAAGAAGTACAAATATGCTATTATGTCGAGAAA 60  
 DB |||||  
 QY 61 ATCTAGAGTGTCCCTCTCTGCGTTGAAGAAGTACAAATATGCTATTATGTCGAGAAA 120  
 DB |||||  
 QY 180 ATCTAGAGTGTCCCTCTCTGCGTTGAAGAAGTACAAATATGCTATTATGTCGAGAAA 239  
 DB |||||  
 QY 121 CACATATTTTGCATAATTTTGCATGCTGAAAATCTTCAACAGAGAAAGAGGCGCTTCAAG 180  
 DB |||||  
 QY 240 CACATATTTTGCATAATTTTGCATGCTGAAAATCTTCAACAGAGAAAGAGGCGCTTCAAG 299  
 DB |||||  
 QY 181 TGTCTTATGTAAGATGATGATATACCAAGAGAGGCTTCAAGAGTAGAGATTTAGT 240  
 DB |||||  
 QY 300 TGTCTTATGTAAGATGATGATATACCAAGAGAGGCTTCAAGAGTAGAGATTTAGT 359  
 DB |||||  
 QY 241 CAACTTGTGAAGAGCTATGAAAATCAATTTGTGCTTTTTCAGCTTTCACAGAGTTGGAG 300  
 DB |||||  
 QY 360 CAACTTGTGAAGAGCTATGAAAATCAATTTGTGCTTTTTCAGCTTTCACAGAGTTGGAG 419  
 DB |||||  
 QY 301 TATGCAAAAGCTATATTTTGCATAATTTTGCATAATTTTGCATAATTTTGCATAATTTTGCATA 360  
 DB |||||  
 QY 420 TATGCAAAAGCTATATTTTGCATAATTTTGCATAATTTTGCATAATTTTGCATAATTTTGCATA 479  
 DB |||||  
 QY 361 GAACTTGTGAAGAGCTATGAAAATCAATTTGTGCTTTTTCAGCTTTCACAGAGTTGGAG 420  
 DB |||||  
 QY 480 GAACTTGTGAAGAGCTATGAAAATCAATTTGTGCTTTTTCAGCTTTCACAGAGTTGGAG 539  
 DB |||||  
 QY 421 GAACTTGTGAAGAGCTATGAAAATCAATTTGTGCTTTTTCAGCTTTCACAGAGTTGGAG 480  
 DB |||||  
 QY 540 GAACTTGTGAAGAGCTATGAAAATCAATTTGTGCTTTTTCAGCTTTCACAGAGTTGGAG 599  
 DB |||||  
 QY 481 ACTGTGAGAGCTCTGAGAGCAAGAGAGGATACCACTTCAAGAGAGGCTTGTCTACATT 540  
 DB |||||  
 QY 600 ACTGTGAGAGCTCTGAGAGCAAGAGAGGATACCACTTCAAGAGAGGCTTGTCTACATT 659  
 DB |||||  
 QY 541 GAACTTGTGAAGAGCTATGAAAATCAATTTGTGCTTTTTCAGCTTTCACAGAGTTGGAG 600  
 DB |||||  
 QY 660 GAACTTGTGAAGAGCTATGAAAATCAATTTGTGCTTTTTCAGCTTTCACAGAGTTGGAG 719  
 DB |||||  
 QY 601 GATCAGAGATTTGTACAAATCACTTCAAGAGAGGATGAAATGAGTTGGATTTCT 660  
 DB |||||  
 QY 720 GATCAGAGATTTGTACAAATCACTTCAAGAGAGGATGAAATGAGTTGGATTTCT 779  
 DB |||||  
 QY 661 GCAAAAGAGGCTCTTGTGAATTTTCTGAGAGCGGATGAAATGAGTTGGATTTCT 720  
 DB |||||



Db 780 GCAAAAAGGCTGCTGTGAATTTCTGAGAGCGATGTAAACMAATCTGAACATCATCA 839  
Qy 721 CCCAGTAAATATGATTTGAACACACCTGAGAGCGTGCAGCTGAGGCGATCCAGAAAG 780  
Db 840 CCCAGTAAATATGATTTGAACACACCTGAGAGCGTGCAGCTGAGGCGATCCAGAAAG 899  
Qy 781 TATCAGGCTAGTCTCTGTTTCAAACTTGCATGTGGAGCCATGTGCAAAATATCTCATGCC 840  
Db 900 TATCAGGCTAGTCTCTGTTTCAAACTTGCATGTGGAGCCATGTGCAAAATATCTCATGCC 959  
Qy 841 AGCTCATATCAGCATGAGAACAGCAGTTTATTACTCACTAAAGACAGAAATGATGTAGAA 900  
Db 960 AGCTCATATCAGCATGAGAACAGCAGTTTATTACTCACTAAAGACAGAAATGATGTAGAA 1019  
Qy 901 AAGGCTGAATTTCTGTATATAAAGCAACAGCCTGGCTTAGCAAGAGCCCAACATAACAGA 960  
Db 1020 AAGGCTGAATTTCTGTATATAAAGCAACAGCCTGGCTTAGCAAGAGCCCAACATAACAGA 1079  
Qy 961 TGGGCTGGAAAGTAAAGAAACATGTATGATAGGCGAATCTCCAGCAGAGAAAGGTTA 1020  
Db 1080 TGGGCTGGAAAGTAAAGAAACATGTATGATAGGCGAATCTCCAGCAGAGAAAGGTTA 1139  
Qy 1021 GATCTGAATCTGATCCCTGTGTGAGAGAAAGAAATGGAATAGCAGAACTGCCATGC 1080  
Db 1140 GATCTGAATCTGATCCCTGTGTGAGAGAAAGAAATGGAATAGCAGAACTGCCATGC 1199  
Qy 1081 TCAGAGAAATCCTAGAGATCTGAAGATGTTCTTGGATAAACATAAATAGCAGATTCAG 1140  
Db 1200 TCAGAGAAATCCTAGAGATCTGAAGATGTTCTTGGATAAACATAAATAGCAGATTCAG 1259  
Qy 1141 AAAGTTAATCAGTGGTTTCCAGAGTGTAGTAACTGTTAGTGTCTGATGACTCACATGAT 1200  
Db 1260 AAAGTTAATCAGTGGTTTCCAGAGTGTAGTAACTGTTAGTGTCTGATGACTCACATGAT 1319  
Qy 1201 GGGGAGTCTGAATCAAAATGCAAGTGTGATTTGGACGTTCTTAAATAGGTTAGAT 1260  
Db 1320 GGGGAGTCTGAATCAAAATGCAAGTGTGATTTGGACGTTCTTAAATAGGTTAGAT 1379  
Qy 1261 GAATATTTCTGGTTCTTCAGAGAAATAGACTTACTGGCAGTGTATCTCATGAGGCTTTA 1320  
Db 1380 GAATATTTCTGGTTCTTCAGAGAAATAGACTTACTGGCAGTGTATCTCATGAGGCTTTA 1439  
Qy 1321 ATATGTAAGAGTCAAGAGGTTTCACTCCAAATCAGTAGAGAGTAAATTTGAAGCAAAATA 1380  
Db 1440 ATATGTAAGAGTCAAGAGGTTTCACTCCAAATCAGTAGAGAGTAAATTTGAAGCAAAATA 1499  
Qy 1381 TTTGGAAACCTTATCGAGAGAGGCAAGCCTCCCAACTTAAGCCATGTAACTGAAAT 1440  
Db 1500 TTTGGAAACCTTATCGAGAGAGGCAAGCCTCCCAACTTAAGCCATGTAACTGAAAT 1559  
Qy 1441 CTAATTTATAGGAGCTTTGTTACTGAGCCACAGATAATACAGAGGCTCCCTCACAAT 1500  
Db 1560 CTAATTTATAGGAGCTTTGTTACTGAGCCACAGATAATACAGAGGCTCCCTCACAAT 1619  
Qy 1501 AAATTAAGCGTAAAGGAGACCTTACATCAGGCTTTTATCTGAGGATTTTATCAAGAAA 1560  
Db 1620 AAATTAAGCGTAAAGGAGACCTTACATCAGGCTTTTATCTGAGGATTTTATCAAGAAA 1679  
Qy 1561 GCAGATTTGGCAGTTCAGAGAGCTCTGAAATGATTAATCAGGAGTAAACCAAGCGAG 1620  
Db 1680 GCAGATTTGGCAGTTCAGAGAGCTCTGAAATGATTAATCAGGAGTAAACCAAGCGAG 1739  
Qy 1621 CAGAAATGGTCAAGTATGATATTTACTAATAGTGGTCAAGAGTAAATAAACAAGGTGAT 1680  
Db 1740 CAGAAATGGTCAAGTATGATATTTACTAATAGTGGTCAAGAGTAAATAAACAAGGTGAT 1799  
Qy 1681 TCTATTCAGAAATGAGAAATCTTACCCAAATAGATCTCTGAAAGAAATCTGCTTTC 1740  
Db 1800 TCTATTCAGAAATGAGAAATCTTACCCAAATAGATCTCTGAAAGAAATCTGCTTTC 1859  
Qy 1741 AAAACCAAGCTGAACTTATAGCAGCAGTATAGCAATATGGAATTCGAAATTAATATC 1800  
Db 1860 AAAACCAAGCTGAACTTATAGCAGCAGTATAGCAATATGGAATTCGAAATTAATATC 1919

Qy 1801 CACAATTTCAAAAGACCTTAAAGAAATAGCGTGGAGGAAGTCTTCTACAGGCATATTT 1860  
Db 1920 CACAATTTCAAAAGACCTTAAAGAAATAGCGTGGAGGAAGTCTTCTACAGGCATATTT 1979  
Qy 1861 CATGCGCTTGAACCTAGTACTAGTAAATCTTAAGCCCACTTAATTTGTACTGAAATGCAA 1920  
Db 1980 CATGCGCTTGAACCTAGTACTAGTAAATCTTAAGCCCACTTAATTTGTACTGAAATGCAA 2039  
Qy 1921 ATTGTAGTGTCTGTAGCAGTGAAGATATAAGAAATTAAGAAATGACAAATGCGAGTC 1980  
Db 2040 ATTGTAGTGTCTGTAGCAGTGAAGATATAAGAAATTAAGAAATGACAAATGCGAGTC 2099  
Qy 1981 AGGCAAGCAGAGAAACCTCAACTCTATGGAAGTAAAGAACTCTGCAACTGGAAGCAAG 2040  
Db 2100 AGGCAAGCAGAGAAACCTCAACTCTATGGAAGTAAAGAACTCTGCAACTGGAAGCAAG 2159  
Qy 2041 AGTAAACAGCCAAATGAACAGACAGTAAAGACATGACAGTGTACTTTTCCAGAGCTG 2100  
Db 2160 AGTAAACAGCCAAATGAACAGACAGTAAAGACATGACAGTGTACTTTTCCAGAGCTG 2219  
Qy 2101 AAGTTAAACAAATGCACTGGTTCTTTTACTTAAGTGTTCAAATACCAAGTGAATTAAGAA 2160  
Db 2220 AAGTTAAACAAATGCACTGGTTCTTTTACTTAAGTGTTCAAATACCAAGTGAATTAAGAA 2279  
Qy 2161 TTTGTCAATCTTAGCCTTCCAAAGAGAGAAAGAAAGAACTAGAAACAGTTAAAGTG 2220  
Db 2280 TTTGTCAATCTTAGCCTTCCAAAGAGAGAAAGAAAGAACTAGAAACAGTTAAAGTG 2339  
Qy 2221 TCTTAATATGCTCAAGAGCCCAAGATCTCATGTTAAGTGGAGAAAGGGTTTTGCAACT 2280  
Db 2340 TCTTAATATGCTCAAGAGCCCAAGATCTCATGTTAAGTGGAGAAAGGGTTTTGCAACT 2399  
Qy 2281 GAAAGATCTGTAGAGTAGCAGTATTTCACTGGTACCTGGTATCTGATTTATGCGACTCAG 2340  
Db 2400 GAAAGATCTGTAGAGTAGCAGTATTTCACTGGTACCTGGTATCTGATTTATGCGACTCAG 2459  
Qy 2341 GAAAGTATCTGTTACTGGAGTTAGCAGTCTTGGGAGAGGCAAAACAGAACCAATAAA 2400  
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Qy 2401 TGTGTAGTCACTGTGCGAGCTTTGAAAACCCCAAGGGACTAATTTCACTGGTTTGTCCAAA 2460  
Db 2520 TGTGTAGTCACTGTGCGAGCTTTGAAAACCCCAAGGGACTAATTTCACTGGTTTGTCCAAA 2579  
Qy 2461 GATATAGAAATGACAGAGAGCTTTAAGTATCCATTTGGGACATGAAGTTAACACAGT 2520  
Db 2580 GATATAGAAATGACAGAGAGCTTTAAGTATCCATTTGGGACATGAAGTTAACACAGT 2639  
Qy 2521 CCGGAAAACAGCATAGAAATGGAAGAGTGAACCTTGATGCTCAGTATTTGCGAGATACA 2580  
Db 2640 CCGGAAAACAGCATAGAAATGGAAGAGTGAACCTTGATGCTCAGTATTTGCGAGATACA 2699  
Qy 2581 TTTCAAGGTTTCAAGCGCAGTCAATTTGCTCTGTTTTCAAAATCCAGGAAATGCAAGAG 2640  
Db 2700 TTTCAAGGTTTCAAGCGCAGTCAATTTGCTCTGTTTTCAAAATCCAGGAAATGCAAGAG 2759  
Qy 2641 GAATGTGCAACATTTCTCTGCCACCTCTGGTCTTTAAAGAAACAAAGTCCAAAAGTCACT 2700  
Db 2760 GAATGTGCAACATTTCTCTGCCACCTCTGGTCTTTAAAGAAACAAAGTCCAAAAGTCACT 2819  
Qy 2701 TTTTGAATGTGAACAAAAGGAGAAATCAAGAGAGAAATGAGTCTTAATATCAAGCCTGTA 2760  
Db 2820 TTTTGAATGTGAACAAAAGGAGAAATCAAGAGAGAAATGAGTCTTAATATCAAGCCTGTA 2879  
Qy 2761 CAGACAGTATATATCAGTGCAGGCTTTCTGTGGTGGTGCAGAAAGATAAGCCAGTTGAT 2820  
Db 2880 CAGACAGTATATATCAGTGCAGGCTTTCTGTGGTGGTGCAGAAAGATAAGCCAGTTGAT 2939  
Qy 2821 AATGCCAAATGTAGTATCAAGAGGAGCTCTAGGTTTTTGTCTATCATCTCAGTTTCAGAGGC 2880  
Db 2940 AATGCCAAATGTAGTATCAAGAGGAGCTCTAGGTTTTTGTCTATCATCTCAGTTTCAGAGGC 2999

Qy	2891	AACGAAACTGGAGCTCATTTACTCCAAATAAAACATGCACTTTTATCAAAACCCATATPCGTATA	2941
Db	3000	AACGAAACTGGAGCTCATTTACTCCAAATAAAACATGCACTTTTATCAAAACCCATATPCGTATA	3059
Qy	2942	CCACCACTTTTCCCACTCAAGCTCATTTGTGTAAABAACTAAATGTAAAGAAAATCTCTCGTAGAG	3000
Db	3060	CCACCACTTTTCCCACTCAAGCTCATTTGTGTAAABAACTAAATGTAAAGAAAATCTCTCGTAGAG	3119
Qy	3001	GAAGAACTTTTGAGGACCAATTCATATGTCACTCGAAAGAGAAAATGGGAAAATGAGAAACATTTCCA	3060
Db	3120	GAAGAACTTTTGAGGACCAATTCATATGTCACTCGAAAGAGAAAATGGGAAAATGAGAAACATTTCCA	3179
Qy	3061	AGTACAGTGAGCACAATTTAGCCGTAAATACATTTAGAGAAAATGTGTTTTAAAGAGGCCAGC	3120
Db	3180	AGTACAGTGAGCACAATTTAGCCGTAAATACATTTAGAGAAAATGTGTTTTAAAGAGGCCAGC	3239
Qy	3121	TCAAGCAATATTTAATGAAGTAGGTTCCAGTACTAATGAAGTGGGCTCCAGTATTAATGAA	3180
Db	3240	TCAAGCAATATTTAATGAAGTAGGTTCCAGTACTAATGAAGTGGGCTCCAGTATTAATGAA	3299
Qy	3181	ATAGGTTCCAGTGATGAAGAAACATTTCAAGCAGAACTAGGTAGAAAACAGAGGCCAAAAATTG	3240
Db	3300	ATAGGTTCCAGTGATGAAGAAACATTTCAAGCAGAACTAGGTAGAAAACAGAGGCCAAAAATTG	3359
Qy	3241	AATGCTATGCTTAGATTAGGGGTTTTGCAACCTCAGGCTCTATAAAACAAAGCTCTTCCTGGA	3300
Db	3360	AATGCTATGCTTAGATTAGGGGTTTTGCAACCTCAGGCTCTATAAAACAAAGCTCTTCCTGGA	3419
Qy	3301	AGTAAATCTGAAGCATCTCGAAAATAAAAAAGCAAGATATCAGAGAGTAGTTCAGACTGTT	3360
Db	3420	AGTAAATCTGAAGCATCTCGAAAATAAAAAAGCAAGATATCAGAGAGTAGTTCAGACTGTT	3479
Qy	3361	AATACAGATTTCTCTCCATATCTCATTTTCAGATAAATTCAGAAACAGGCTATGGCAAGTAGT	3420
Db	3480	AATACAGATTTCTCTCCATATCTCATTTTCAGATAAATTCAGAAACAGGCTATGGCAAGTAGT	3539
Qy	3421	CATGCATCTCAGGTTTGTTCGAGACAACCTGATGACCTGTTTAGATGATGTGGAATAAAG	3480
Db	3540	CATGCATCTCAGGTTTGTTCGAGACAACCTGATGACCTGTTTAGATGATGTGGAATAAAG	3599
Qy	3481	GAAGATACTAGTTTGTCTGAAAATGACATTAAGAAAAGTTCTGCTGTTTTTATGCAAAAGC	3540
Db	3600	GAAGATACTAGTTTGTCTGAAAATGACATTAAGAAAAGTTCTGCTGTTTTTATGCAAAAGC	3659
Qy	3541	GTCCAGAGAGGAGAGCTTAGCAGGAGTCTCAGCCCTTTCCACCATACACATTTGGCTCAG	3600
Db	3660	GTCCAGAGAGGAGAGCTTAGCAGGAGTCTCAGCCCTTTCCACCATACACATTTGGCTCAG	3719
Qy	3601	GGTTACCGAGAGGGGCGAAGAAATTAGAGTCTCTCAGAGAGAACTTATCTAGTAGAGAT	3660
Db	3720	GGTTACCGAGAGGGGCGAAGAAATTAGAGTCTCTCAGAGAGAACTTATCTAGTAGAGAT	3779
Qy	3661	GAAGAGCTTCCCTGCTTCCAAACACTTGCTATTTTGGTAAAGTAAACAATATACCTTCTCAG	3720
Db	3780	GAAGAGCTTCCCTGCTTCCAAACACTTGCTATTTTGGTAAAGTAAACAATATACCTTCTCAG	3839
Qy	3721	TCTACTAGGCATAGCAACGGTTGCTACCGAGTGCTGTCTAAGAAACACAGAGAGAAATTTA	3780
Db	3840	TCTACTAGGCATAGCAACGGTTGCTACCGAGTGCTGTCTAAGAAACACAGAGAGAAATTTA	3899
Qy	3781	TTATCATTTGAAGAAATAGCTTAAATGACTGCAGATTAACCCAGGTAAATATTTGGCAAAAGGCATCT	3840
Db	3900	TTATCATTTGAAGAAATAGCTTAAATGACTGCAGATTAACCCAGGTAAATATTTGGCAAAAGGCATCT	3959
Qy	3841	CAGGAACATCACCTTAGTGAGGAAACAAAATGTTCTGCTAGCTTGTTTCTTCCACAGTGC	3900
Db	3960	CAGGAACATCACCTTAGTGAGGAAACAAAATGTTCTGCTAGCTTGTTTCTTCCACAGTGC	4019
Qy	3901	AGTGAATTTGGAAGACTTGACTGCAATATACAAAACCCAGGATCCTTCTTGATTTGGTCTCT	3960
Db	4020	AGTGAATTTGGAAGACTTGACTGCAATATACAAAACCCAGGATCCTTCTTGATTTGGTCTCT	4079
Qy	3961	TCCAAAACAAATGAGGGCATGACTGTGAAGAGCCAGGGAGTTGGTCTGAGTGAACAGGAATTG	4020

Db 5160 ACTGAAGAGACTACTCATGTTGTTATGAAACAGATGCTGAGTTTGTGTGAACGGACA 5219  
 Qy 5101 CTGAATAATTTTCTAGGAATTCGGGAGGAAATAGGTTAGTACTATTCTCGGTGACC 5160  
 Db 5220 CTGAATAATTTTCTAGGAATTCGGGAGGAAATAGGTTAGTACTATTCTCGGTGACC 5279  
 Qy 5161 CAGTCTATTAAAGAAAGAAATGCTGAATCAGCATGATTTTGAAGTCAGAGGAGATGTG 5220  
 Db 5280 CAGTCTATTAAAGAAAGAAATGCTGAATCAGCATGATTTTGAAGTCAGAGGAGATGTG 5339  
 Qy 5221 GTCATATGAAGAAACCAACAGGTCCAAAGCGAGCAAGAGATCCAGGACAGAAAGATC 5280  
 Db 5340 GTCATATGAAGAAACCAACAGGTCCAAAGCGAGCAAGAGATCCAGGACAGAAAGATC 5399  
 Qy 5281 TTCAGGGGGCTAGAAATCTGTTGCTATGCGGCCCTTCCACACATGSCCCACAGATCAACTG 5340  
 Db 5400 TTCAGGGGGCTAGAAATCTGTTGCTATGCGGCCCTTCCACACATGSCCCACAGATCAACTG 5459  
 Qy 5341 GAATGATGTGTACAGCTGTGTGCTCTGTGTGAGGAGCTTTTCATCATCCACCTT 5400  
 Db 5460 GAATGATGTGTACAGCTGTGTGCTCTGTGTGAGGAGCTTTTCATCATCCACCTT 5519  
 Qy 5401 GGCACAGGTGTCACCCCAATTTGTTGTGCGAGCAGATGCTGTGACAGAGGCAATGGC 5460  
 Db 5520 GGCACAGGTGTCACCCCAATTTGTTGTGCGAGCAGATGCTGTGACAGAGGCAATGGC 5579  
 Qy 5461 TTCATGCAATTTGGGCGAGATGTGTGAGGCACCTGTGTGTGACCCGAGAGTGGTGTGGAC 5520  
 Db 5580 TTCATGCAATTTGGGCGAGATGTGTGAGGCACCTGTGTGTGACCCGAGAGTGGTGTGGAC 5639  
 Qy 5521 AGTGTAGACTCTACAGAGTCCAGAGTGTGACACTTACCTGATACCCAGATCCCCAC 5580  
 Db 5640 AGTGTAGACTCTACAGAGTCCAGAGTGTGACACTTACCTGATACCCAGATCCCCAC 5699  
 Qy 5581 AGCCACTAC 5589  
 Db 5700 AGCCACTAC 5708  
 RESULT 12  
 ID AAV46471 standard; cDNA; 5711 BP.  
 XX AAV46471;  
 AC AAV46471;  
 XX 18-NOV-1998 (first entry)  
 XX Human BRCA1 omi3 polymorphism #7 cDNA.  
 KW BRCA1; omi3; human; breast and ovarian cancer predisposing gene;  
 KW polymorphism; susceptibility; anti-oncogene; tumour suppressor;  
 KW chromosome 17q; ss.  
 XX Homo sapiens.  
 XX Key Location/Qualifiers  
 XX CDS 120..5711  
 XX /\*tag= a  
 XX /product= "BRCA1 omi3 protein"  
 XX variation 4956  
 XX /\*tag= b  
 XX /note= "This polymorphic variation can be an A or G  
 XX nucleotide"  
 XX US5750400-A.  
 XX 12-MAY-1998.  
 XX 12-FEB-1997; 97US-00798691.  
 XX 12-FEB-1996; 96US-00598591.  
 XX (ONCO-) ONCORMED INC.

XX Olson SJ, Murphy PD, Zeng B, Alvares CP, Schelter DB, Allen AC;  
 PI Critz BS;  
 XX WPI; 1998-296774/26.  
 XX BRCA1 omi gene coding sequences - useful for distinguishing between  
 PT polymorphisms and mutation(s) in the screening for disposition to breast  
 PT or ovarian cancer.  
 XX Claim 2e; Page; 54pp; English.  
 XX This sequence encodes a human BRCA1 (breast and ovarian cancer  
 CC predisposing gene) omi3 gene in which a polymorphic variation occurs at  
 CC nucleotide 4956. This sequence and other polymorphic variations of this  
 CC sequence are useful for the identification of an individual who may or  
 CC may not have an increased susceptibility to breast or ovarian cancer. The  
 CC sequences used identify gene changes which are due to polymorphisms,  
 CC rather than cancer causing mutations. BRCA1 is an anti-oncogene (tumour  
 CC suppressor) which is involved in genetic inheritance of cancers,  
 CC especially breast and ovarian cancer. It is found at human chromosome 17q  
 CC which is known to be linked to cancer susceptibility, especially breast  
 CC cancer. Cells containing a mutation in this gene lose the wild-type  
 CC function of BRCA1 and are more susceptible to cancers. NOTE: This  
 CC sequence does not appear in the specification but has been created from  
 CC the wild type BRCA1 omi3 gene represented in AAV46450  
 XX  
 SQ Sequence 5711 BP; 1953 A; 1098 C; 1276 G; 1383 T; 0 U; 1 Other;  
 Query Match 100.0%; Score 5588.6; DB 2; Length 5711;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 5588; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 ATGATTTATCTGCTCTGCGTGAAGAAAGTACAAAATGTCAATTAATGTATGCAGAAA 60  
 Db 120 ATGATTTATCTGCTCTGCGTGAAGAAAGTACAAAATGTCAATTAATGTATGCAGAAA 179  
 Qy 61 ATCTTAGAGTGCCCATCTGCTGAGAGTTGATCAAGAAACCTGTCTCCCAAAAGTGTGAC 120  
 Db 180 ATCTTAGAGTGCCCATCTGCTGAGAGTTGATCAAGAAACCTGTCTCCCAAAAGTGTGAC 239  
 Qy 121 CACATATTTGCAAAATTTTGGCATGCTGAAACTTCTCAACAGAGAAAGGGCTTCACAG 180  
 Db 240 CACATATTTGCAAAATTTTGGCATGCTGAAACTTCTCAACAGAGAAAGGGCTTCACAG 299  
 Qy 181 TGTCTTTATGTAAGATGATATACCAAAAGAGGCTTACAAAGAAAGTACGAGATTAGT 240  
 Db 300 TGTCTTTATGTAAGATGATATACCAAAAGAGGCTTACAAAGAAAGTACGAGATTAGT 359  
 Qy 241 CAACTTGTGAGAGCTATTGAAATCAATTTGCTTTTTCAGCTTGACACAGGTTGGAG 300  
 Db 360 CAACTTGTGAGAGCTATTGAAATCAATTTGCTTTTTCAGCTTGACACAGGTTGGAG 419  
 Qy 301 TATGCAAAACAGCTATAAATTTTGCAAAAGAGGAAATACTCTCTGAAACATCTAAAGAT 360  
 Db 420 TATGCAAAACAGCTATAAATTTTGCAAAAGAGGAAATACTCTCTGAAACATCTAAAGAT 479  
 Qy 361 GAAGTTTCTATCATCAAAAGTATGGCTTACAGAAACCGTGCAGAAAGCTTCTACAGAT 420  
 Db 480 GAAGTTTCTATCATCAAAAGTATGGCTTACAGAAACCGTGCAGAAAGCTTCTACAGAT 539  
 Qy 421 GAACCGGAAATCTCTTCTGAGGAAACAGTCTCAGTGTCCAACTCTTAACCTTGA 480  
 Db 540 GAACCGGAAATCTCTTCTGAGGAAACAGTCTCAGTGTCCAACTCTTAACCTTGA 599  
 Qy 481 ACTGTGAGAACTCTGAGGAAAGAGGAGATACAACTCAAAAGAGCGTCTGTCTACATT 540  
 Db 600 ACTGTGAGAACTCTGAGGAAAGAGGAGATACAACTCAAAAGAGCGTCTGTCTACATT 659  
 Qy 541 GAATTGGGATCTGATTCTTCTGAAGATACCGTTAATAGGCAACTTATTGCGAGTGGGA 600  
 Db 660 GAATTGGGATCTGATTCTTCTGAAGATACCGTTAATAGGCAACTTATTGCGAGTGGGA 719

QY 601 GATCAGAAATGTTTACAAATCACCCTCAGAGAAACCAAGGATGAATCAGTTGGATTCT 660  
DB 720 GATCAGAAATGTTTACAAATCACCCTCAGAGAAACCAAGGATGAATCAGTTGGATTCT 779  
QY 661 GCAAAAAGGCTGCTTGTGAATTTCTGACAGCGATGTAAACAATAGTGAACATCATCAA 720  
DB 780 GCAAAAAGGCTGCTTGTGAATTTCTGACAGCGATGTAAACAATAGTGAACATCATCAA 839  
QY 721 CCAGTAAATGATTTGAACACACCTGAGAGAGCGTGCAGCTGAGAGGCAATCCAGAAAG 780  
DB 840 CCCAGTAAATGATTTGAACACACCTGAGAGAGCGTGCAGCTGAGAGGCAATCCAGAAAG 899  
QY 781 TATCAGGCTAGTCTCTGTTTCAAACTTCGATGAGAGCAATGTGCAACAATACTCATGCC 840  
DB 900 TATCAGGCTAGTCTCTGTTTCAAACTTCGATGAGAGCAATGTGCAACAATACTCATGCC 959  
QY 841 AGCTCATTTACAGCATGAGAACAGCAGTGTATTAATCTCACTAAAGCAGAAATGTAGAA 900  
DB 960 AGCTCATTTACAGCATGAGAACAGCAGTGTATTAATCTCACTAAAGCAGAAATGTAGAA 1019  
QY 901 AAGGCTGAATTTCTGTAATAAAGCAACAGCCTGGCTTAGCAAGGAGCCAACTAAACAGA 960  
DB 1020 AAGGCTGAATTTCTGTAATAAAGCAACAGCCTGGCTTAGCAAGGAGCCAACTAAACAGA 1079  
QY 961 TGGCTCGAAGTAAAGGAAACATGTAATGATAGGCGGACTCCAGCAAGAAAAAGGTA 1020  
DB 1080 TGGCTCGAAGTAAAGGAAACATGTAATGATAGGCGGACTCCAGCAAGAAAAAGGTA 1139  
QY 1021 GATCTGAATGCTGATCCCTGCTGTGAGAGAAAGAAATGGATAGCAGAACTGCCATGC 1080  
DB 1140 GATCTGAATGCTGATCCCTGCTGTGAGAGAAAGAAATGGATAGCAGAACTGCCATGC 1199  
QY 1081 TCAGAGAACTCCTAGAGTACTGAAGATGTTCTTTGGATAACAATAAGCAGCATTCAG 1140  
DB 1200 TCAGAGAACTCCTAGAGTACTGAAGATGTTCTTTGGATAACAATAAGCAGCATTCAG 1259  
QY 1141 AAGGTTAATGAGTGGTTTCCAGAGTGAATGATGATGTTAGTCTGATGATCTCAGATGAT 1200  
DB 1260 AAGGTTAATGAGTGGTTTCCAGAGTGAATGATGATGTTAGTCTGATGATCTCAGATGAT 1319  
QY 1201 GGGAGTCTGAATCAAAATGCCAAATAGTCTGATGATGTTTGAAGCGTTCTAAATGAGGTAGAT 1260  
DB 1320 GGGAGTCTGAATCAAAATGCCAAATAGTCTGATGATGTTTGAAGCGTTCTAAATGAGGTAGAT 1379  
QY 1261 GAATATTCGTTCTTCAGAGAAATAGACTTACTGCCAGTGTATCTCATGAGGCTTTA 1320  
DB 1380 GAATATTCGTTCTTCAGAGAAATAGACTTACTGCCAGTGTATCTCATGAGGCTTTA 1439  
QY 1321 ATATGTAAGTGAAGAGTTCACTCCAAATCAGTAGAGATGATATTTGAAGCAAAATA 1380  
DB 1440 ATATGTAAGTGAAGAGTTCACTCCAAATCAGTAGAGTATATTTGAAGCAAAATA 1499  
QY 1381 TTTGGGAAACCTATCGGAAGAGGCAAGCTCCCAACTTAAGCCATGTAACTGAAAT 1440  
DB 1500 TTTGGGAAACCTATCGGAAGAGGCAAGCTCCCAACTTAAGCCATGTAACTGAAAT 1559  
QY 1441 CTAATTAAGGAGCAATTTGTTACTGAGCCACAGATATAACAGAGCGTCCCTCACAAT 1500  
DB 1560 CTAATTAAGGAGCAATTTGTTACTGAGCCACAGATATAACAGAGCGTCCCTCACAAT 1619  
QY 1501 AAATTAAGCGTAAAGGAGACTTACATCAGGCTTTCATCTGAGGATTTTATCAAGAAA 1560  
DB 1620 AAATTAAGCGTAAAGGAGACTTACATCAGGCTTTCATCTGAGGATTTTATCAAGAAA 1679  
QY 1561 GCAGATTCGAGTTCAAAAGACTCCGTAATGATGATGATGATGATGATGATGATGATGAT 1620  
DB 1680 GCAGATTCGAGTTCAAAAGACTCCGTAATGATGATGATGATGATGATGATGATGATGAT 1739  
QY 1621 CAGAAATGCTCAAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1680  
DB 1740 CAGAAATGCTCAAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1799  
QY 1681 TCTATTAGATGAGAAAAATCCTTAACCCCAATAGATCACTCGAAAAAGAAATCTGCTTTC 1740

DB 1800 TCTATTAGATGAGAAAAATCCTTAACCCCAATAGATCACTCGAAAAAGAAATCTGCTTTC 1859  
QY 1741 AAAACGAAAGCTGAACCTATAAGCAGCAGTATAAGCAATATGAACTCGAATTAATATC 1800  
DB 1860 AAAACGAAAGCTGAACCTATAAGCAGCAGTATAAGCAATATGAACTCGAATTAATATC 1919  
QY 1801 CCAATTTCAAAAGCACCCTAAAGAAATAGGCTGAGAGGAACTCTTCTACAGGCAATTT 1860  
DB 1920 CCAATTTCAAAAGCACCCTAAAGAAATAGGCTGAGAGGAACTCTTCTACAGGCAATTT 1979  
QY 1861 CATGCCCTTGAACCTAGTACTAGTAGAAATCTAAGCCCACTAAATTTGTAATGTAATTC 1920  
DB 1980 CATGCCCTTGAACCTAGTACTAGTAGAAATCTAAGCCCACTAAATTTGTAATGTAATTC 2039  
QY 1921 ATTGATAGTGTCTTAGCAGTGAAGATAAAGAAAAAAGTACACCAATGCCAGTC 1980  
DB 2040 ATTGATAGTGTCTTAGCAGTGAAGATAAAGAAAAAAGTACACCAATGCCAGTC 2099  
QY 1981 AGSCACAGCAGAAACCTACAACTCATGGAAGGTAAAGAACTCTGCAACTGGAGCCAGAAAG 2040  
DB 2100 AGSCACAGCAGAAACCTACAACTCATGGAAGGTAAAGAACTCTGCAACTGGAGCCAGAAAG 2159  
QY 2041 AGTACACAGCCAAATGAACAGACAAAGTAAAGACATGACAGTATCTTTCCAGAGCTG 2100  
DB 2160 AGTAAACAGCCAAATGAACAGACAAAGTAAAGACATGACAGTATCTTTCCAGAGCTG 2219  
QY 2101 AAGTTAAACAAATGACCTGTTCTTTTACTAGTGTTCATAATACCAAGTGAATTTAAAGAA 2160  
DB 2220 AAGTTAAACAAATGACCTGTTCTTTTACTAGTGTTCATAATACCAAGTGAATTTAAAGAA 2279  
QY 2161 TTTGTCATCTTAGAGCTTCCAAAGAGAAAGAAAGAGAGAACTAGAAACAGTTTAAAGTG 2220  
DB 2280 TTTGTCATCTTAGAGCTTCCAAAGAGAAAGAAAGAGAGAACTAGAAACAGTTTAAAGTG 2339  
QY 2221 TCTTAATAAGTCTGAGAGCCCAAGGTCATGTTTAAAGTGAAGAGGTTTTCGAAACT 2280  
DB 2340 TCTTAATAAGTCTGAGAGCCCAAGGTCATGTTTAAAGTGAAGAGGTTTTCGAAACT 2399  
QY 2281 GAAAGATCTGTAGAGAGTACAGTATTTCACTGGTACCTGGTACTGATTTATGGCACTCAG 2340  
DB 2400 GAAAGATCTGTAGAGAGTACAGTATTTCACTGGTACCTGGTACTGATTTATGGCACTCAG 2459  
QY 2341 GAAAGTATCTGTTACTGGAAGTACCTCTAGGAGAGGCAAAACAGAACCAATATA 2400  
DB 2460 GAAAGTATCTGTTACTGGAAGTACCTCTAGGAGAGGCAAAACAGAACCAATATA 2519  
QY 2401 TGTGTGAGTCAAGTGTGAGCAATTTGAAACCCCAAGGGACTAATTCATGTTTGTTCGAA 2460  
DB 2520 TGTGTGAGTCAAGTGTGAGCAATTTGAAACCCCAAGGGACTAATTCATGTTTGTTCGAA 2579  
QY 2461 GATAATGAAATGACACAGAGCGTTTAAAGTATCCATTGGGACATGAGTTTAAACAGT 2520  
DB 2580 GATAATGAAATGACACAGAGCGTTTAAAGTATCCATTGGGACATGAGTTTAAACAGT 2639  
QY 2521 CGGGAACCAAGCATAGAAATGGAAGAAAGTAACTGATGCTCAGTATTTGAGAGATACA 2580  
DB 2640 CGGGAACCAAGCATAGAAATGGAAGAAAGTAACTGATGCTCAGTATTTGAGAGATACA 2699  
QY 2581 TTCAGGTTTCAAGGCGCAGTCATTTGCTCTGTTTTTCAATCCAGGAAATCGAGAGAG 2640  
DB 2700 TTCAGGTTTCAAGGCGCAGTCATTTGCTCTGTTTTTCAATCCAGGAAATCGAGAGAG 2759  
QY 2641 GAATGTCAACATCTCTGCCACTCTGGGTCTTCTTAAAGAAACAAAGTCCAAAGTCACT 2700  
DB 2760 GAATGTCAACATCTCTGCCACTCTGGGTCTTCTTAAAGAAACAAAGTCCAAAGTCACT 2819  
QY 2701 TTTGAATGTGAACAAAGGAGAAATCAAGGAAAGTAACTAGTCTTAATATCAAGCTGTA 2760  
DB 2820 TTTGAATGTGAACAAAGGAGAAATCAAGGAAAGTAACTAGTCTTAATATCAAGCTGTA 2879  
QY 2761 CAGACAGTTAATATCACTGAGGCTTCTGTTGGTTCAGAAAGATAGGAGGCTGAT 2820

Db 2880 CAGCAGATTATATCATCTGAGGCTTTCCTGTGTGGTTCAGAAAGATAAGCCAGTTGAT 2839  
Qy 2821 AATGCCAAATGTAGTATCAAGAGGAGGCTCTAGGTTTGTCTATCATCTCAGTTTCAGAGGC 2880  
Db 2940 AATGCCAAATGTAGTATCAAGAGGAGGCTCTAGGTTTGTCTATCATCTCAGTTTCAGAGGC 2999  
Qy 2881 AACGAACTGGAGCTCATTTACTCCAAATATAACATGAGCTTTTACAAACCCATATCGTATA 2940  
Db 3000 AACGAACTGGAGCTCATTTACTCCAAATATAACATGAGCTTTTACAAACCCATATCGTATA 3059  
Qy 2941 CCACCACCTTTTCCCATCAAGTCAATTTGTTAAATCTAAATGTAAAGAAAAATCTGCTAGAG 3000  
Db 3060 CCACCACCTTTTCCCATCAAGTCAATTTGTTAAATCTAAATGTAAAGAAAAATCTGCTAGAG 3119  
Qy 3001 GAAAACTTTTCAGGACACATTCATGTCACCTGGAAGAGAAATGGAAATGGAATGGAACATTCGA 3060  
Db 3120 GAAAACTTTTCAGGACACATTCATGTCACCTGGAAGAGAAATGGAAATGGAATGGAACATTCGA 3179  
Qy 3061 AGTACAGTGAAGCAATTTAGCCGTAATTAACATTTAGAGAAATGTTTAAAGGAGCCAGC 3120  
Db 3180 AGTACAGTGAAGCAATTTAGCCGTAATTAACATTTAGAGAAATGTTTAAAGGAGCCAGC 3239  
Qy 3121 TCAAGCAATTAATTAAGTAGTGTTCAGTACTAATTAAGTAGTGGCTCCAGTATTAATGA 3180  
Db 3240 TCAAGCAATTAATTAAGTAGTGTTCAGTACTAATTAAGTAGTGGCTCCAGTATTAATGA 3299  
Qy 3181 ATAGGTTCCAGTGAATGAATAATCAAGCAGAACTAGTGTAAACAGAGGGCCAAATTTG 3240  
Db 3300 ATAGGTTCCAGTGAATGAATAATCAAGCAGAACTAGTGTAAACAGAGGGCCAAATTTG 3359  
Qy 3241 AATGCTATGCTTAGATTAGGGTTTTCGAACTGAGGTCTATAAAACAAAGTCTTCCTGGA 3300  
Db 3360 AATGCTATGCTTAGATTAGGGTTTTCGAACTGAGGTCTATAAAACAAAGTCTTCCTGGA 3419  
Qy 3301 AGTAATTTGAAGCATCTGAAATTAATAAAGACAGAGATATGAAGTAGTTTCAGAGCTGTT 3360  
Db 3420 AGTAATTTGAAGCATCTGAAATTAATAAAGACAGAGATATGAAGTAGTTTCAGAGCTGTT 3479  
Qy 3361 AATACAGATTCTCTCCATATCTGATTTCAGATAAATCTAGAAACAGGCTATGGGAAGTAGT 3420  
Db 3480 AATACAGATTCTCTCCATATCTGATTTCAGATAAATCTAGAAACAGGCTATGGGAAGTAGT 3539  
Qy 3421 CATGCTATCAGGTTTGTCTGAGACACCTGATGACCTGTATGATGATGATGATGATGATGAT 3480  
Db 3540 CATGCTATCAGGTTTGTCTGAGACACCTGATGACCTGTATGATGATGATGATGATGATGAT 3599  
Qy 3481 GAAGATACTAGTTTGTCTGAAATGACATTTAAGAAAGTTCTGCTGTTTTCAGCAAAAGC 3540  
Db 3600 GAAGATACTAGTTTGTCTGAAATGACATTTAAGAAAGTTCTGCTGTTTTCAGCAAAAGC 3659  
Qy 3541 GTCCAGAGAGGAGCTTAGCAGAGTCTTAGGCCCTTTCACCCATACACATTTGGCTCAG 3600  
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Qy 3601 GGTTCACGAGAGGGGCCAAGAAATTAGAGTCTCTCAGAGAGAACTTATCTAGTAGGAGAT 3660  
Db 3720 GGTTCACGAGAGGGGCCAAGAAATTAGAGTCTCTCAGAGAGAACTTATCTAGTAGGAGAT 3779  
Qy 3661 GAAGAGCTTCCCTGCTTCAACACTGTTATTGTTAAAGTAAACAAATATACCTTCTCAG 3720  
Db 3780 GAAGAGCTTCCCTGCTTCAACACTGTTATTGTTAAAGTAAACAAATATACCTTCTCAG 3839  
Qy 3721 TCTACTAGGAGATAGCAGGCTTACCGAGTGTCTCTTAAGAAACACAGAGAGAAATTTA 3780  
Db 3840 TCTACTAGGAGATAGCAGGCTTACCGAGTGTCTCTTAAGAAACACAGAGAGAAATTTA 3899  
Qy 3781 TTATCATTTGAAGATAGCTTAAATGATCTCAGTAACCAAGTAAATTTGCAAGGCACTCT 3840  
Db 3900 TTATCATTTGAAGATAGCTTAAATGATCTCAGTAACCAAGTAAATTTGCAAGGCACTCT 3959  
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Db 3960 CAGGAACATCACTTAGTGAAGAAACAAATGTTCTGCTAGCTGTTTCTTCTCAGCTGC 4019

Qy 3901 AGTGAATTGGAAGACTTGACTGCAATAACAACACCCAGAGATCTTTTCTTGATTTGTTCT 3960  
Db 4020 AGTGAATTGGAAGACTTGACTGCAATAACAACACCCAGAGATCTTTTCTTGATTTGTTCT 4079  
Qy 3961 TCCAAACAAATCAGGACATCAGTCTGAAAGCCAGGAGTTGTTGCTGAGTCAAGGAATTTG 4020  
Db 4080 TCCAAACAAATCAGGACATCAGTCTGAAAGCCAGGAGTTGTTGCTGAGTCAAGGAATTTG 4139  
Qy 4021 GTTTCAGATGATGAAGAAAGAGAAACGGCTTTGGAAGAAAAATAATCAAGAAAGCAAGC 4080  
Db 4140 GTTTCAGATGATGAAGAAAGAGAAACGGCTTTGGAAGAAAAATAATCAAGAAAGCAAGC 4199  
Qy 4081 ATGGATTCAAACTTAGTGAAGCAGCATCTGAGTGTGAGAGTGAACAGAGCTCTCTGAA 4140  
Db 4200 ATGGATTCAAACTTAGTGAAGCAGCATCTGAGTGTGAGAGTGAACAGAGCTCTCTGAA 4259  
Qy 4141 GACTCTCAGGCTATCTCTCAGAGTGAACATTTTAAACCACTCAGCAGAGGATACCATG 4200  
Db 4260 GACTCTCAGGCTATCTCTCAGAGTGAACATTTTAAACCACTCAGCAGAGGATACCATG 4319  
Qy 4201 CAACTAACCTGATTAAGCTCCAGCAGGAAATGGCTGAACCTAGAGCTGTGTAGACAG 4260  
Db 4320 CAACTAACCTGATTAAGCTCCAGCAGGAAATGGCTGAACCTAGAGCTGTGTAGACAG 4379  
Qy 4261 CATGGAGCCAGCTTCTAAACAGCTACCTTCCATCATAAAGTGAATCTTCTGCCCTTGAG 4320  
Db 4380 CATGGAGCCAGCTTCTPAACAGCTACCTTCCATCATAAAGTGAATCTTCTGCCCTTGAG 4439  
Qy 4321 GACCTGCGAAATCCAGAACAAAGACATCAGAAAAAGCGATTAATTAATTCACAGAAAGT 4380  
Db 4440 GACCTGCGAAATCCAGAACAAAGACATCAGAAAAAGCGATTAATTAATTCACAGAAAGT 4499  
Qy 4381 AGTGAATACCTTATAAGCCAGAAATCCAGAGGCCCTTTCTGCTGACAAAGTTTCAGGTCT 4440  
Db 4500 AGTGAATACCTTATAAGCCAGAAATCCAGAGGCCCTTTCTGCTGACAAAGTTTCAGGTCT 4559  
Qy 4441 CGAGATAGTTCTACAGTAAATAAAGAAACAGAGTGGAAAGTCAATCCCTCTCTAAA 4500  
Db 4560 CGAGATAGTTCTACAGTAAATAAAGAAACAGAGTGGAAAGTCAATCCCTCTCTAAA 4619  
Qy 4501 TGCCCATCATTAGATGATAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 4560  
Db 4620 TGCCCATCATTAGATGATAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 4679  
Qy 4561 AATACCATCTCAAGAGAGCTCAATTAAGGTTGTTGATGATGATGATGATGATGATGATGATGAT 4620  
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Qy 4621 GAGTCTGGGCCACACAGATTTGCGAAACATCTTACTTCCAGAGGAGCAATCTAGAGGA 4680  
Db 4740 GAGTCTGGGCCACACAGATTTGCGAAACATCTTACTTCCAGAGGAGCAATCTAGAGGA 4799  
Qy 4681 ACCCTTACCTTGGAACTCTGGAATCAGCTCTTCTCTGATGATGATGATGATGATGATGATGATGAT 4740  
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Qy 4741 GAAGACAGAGCCCGCAGAGTCTGCTGTGTTGGGAAACATACCATCTTCAACCTCTGCAATG 4800  
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Qy 4801 AAAGTTTCCCAATTTGAAGTTGCAAGATCTGCCAGGGTCCAGCTGTGCTCATACTACT 4860  
Db 4920 AAAGTTTCCCAATTTGAAGTTGCAAGATCTGCCAGGGTCCAGCTGTGCTCATACTACT 4979  
Qy 4861 GATCTGCTGGGTATAATGCAATGGAAGAAAGTGTGAGCAGGGGAAAGCCAGAAATTTGACA 4920  
Db 4980 GATCTGCTGGGTATAATGCAATGGAAGAAAGTGTGAGCAGGGGAAAGCCAGAAATTTGACA 5039  
Qy 4921 GCTTCAACAGAAAGGTTCAACAAAGAAATCTCCATGTTGGTGTCTTGGGCTGACCCAGAA 4980  
Db 5040 GCTTCAACAGAAAGGTTCAACAAAGAAATCTCCATGTTGGTGTCTTGGGCTGACCCAGAA 5099

QY 4981 GAAATTTATGCTCGGTACAAAGTTTCCAGAAACACACATCATCTTTAACTAATCTAATT 5040  
Db 5100 GAAATTTATGCTCGGTACAAAGTTTCCAGAAACACACATCATCTTTAACTAATCTAATT 5159  
QY 5041 ACTCAAGAGACTACTCATGTTGTTATGAAGACAGAGCTGAGTTTGTGTGAACGACGA 5100  
Db 5160 ACTCAAGAGACTACTCATGTTGTTATGAAGACAGAGCTGAGTTTGTGTGAACGACGA 5219  
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Db 5280 CAGTCTATTAAGAAAGAAATGCTGAATGAGCATGATTTTGAATGACAGAGAGTGTG 5339  
QY 5221 GTCAATGGAAGAACACCAAGGTCCTCAAGCGACAGAGAAATCCCAAGGACAGAAATGC 5280  
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QY 5281 TTCAAGGGGGTAGAAATCTGTGTTATGAGGCGCTTCAACCAATGCCCACAGATCAACTG 5340  
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QY 5341 GAATGATGTACAGCTGTGTGCTTCTCTGTGTGAGGAGCTTTCATCATCACTCCCTT 5400  
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Db 5640 AGTGTAGCACTTACCAAGTGCAGGAGCTGCACACCTTACCTGATACCCAGATCCGCCAC 5699  
QY 5581 AGCCACTAC 5589  
Db 5700 AGCCACTAC 5708  
RESULT 13  
AAT87085  
ID AAT87085 standard; cDNA; 5711 BP.  
AC AAT87085;  
DT 06-JAN-1998 (first entry)  
DE Human BRCA1 gene consensus.  
XX BRCA1 gene; BRCA1(omi); breast cancer; ovary cancer; polymorphism;  
XX genetic testing; diagnosis; gene therapy; ss.  
XX Homo sapiens.  
FH Key Location/Qualifiers  
FT CDS 120..5711  
FT variation /\*tag= a  
FT 2201  
FT /\*tag= b  
FT /note= "AGC (40%) and AGT (55-65%) polymorphism at  
FT position 2201"  
FT 2430  
FT variation /\*tag= c  
FT /note= "35-45% TGG (Leu) and 55-65% CTG (Leu)  
FT polymorphism at position 2430"  
FT 2731  
FT variation /\*tag= d

FT variation /note= "25-35% CCG (Pro) and 65-75% CTG (Leu)  
3232  
FT /\*tag= e  
FT /note= "35-45% GAA (Glu) and 55-65% GGA (Gly)  
3667  
FT polymorphism at position 3232"  
FT /\*tag= f  
FT /note= "35-45% AAA (Lys) and 55-63% AGA (Arg)  
4427  
FT polymorphism at position 3667"  
FT /\*tag= g  
FT /note= "45-55% TCT (Ser) and 45-55% TCC (Ser)  
4956  
FT polymorphism at position 4427"  
FT /\*tag= h  
FT /note= "35-45% AGT (Ser) and 55-65% GGT (Gly)  
polymorphism at position 4956"  
US5654155-A.  
05-AUG-1997.  
12-FEB-1996; 96US-00598591.  
12-FEB-1996; 96US-00598591.  
{ONCO-} ONCORMED INC.  
Olson SJ, Allen AC, Zeng B, Schelter DB, Alvares CP, Murphy PD;  
Critz BS;  
WPI; 1997-401843/37.  
P-PSDB; AAW26522.  
Human BRCA1 gene coding sequence with common normal polymorphisms - for  
assessing susceptibility to breast or ovarian cancer.  
Claim 1; Col 19-24; 35pp; English.  
This nucleotide sequence comprises a consensus DNA sequence, designated  
BRCA1(omi), for the normal human BRCA1 gene. It was found by end-to-end  
sequencing of the BRCA1 gene from 5 individuals randomly drawn from the  
population and found to have no family history of breast or ovarian  
cancer. The BRCA1(omi) gene and the seven polymorphic sites (which are  
not associated with breast or ovarian cancer) will provide greater  
accuracy and reliability for genetic testing. A claimed method for  
detecting an increased genetic susceptibility to breast and ovarian  
cancer resulting from the presence of a mutation in the BRCA1 coding  
sequence involves amplifying and sequencing the BRCA1 coding sequence  
from an individual and comparing the sequence with BRCA1(omi). The  
consensus normal BRCA1 sequence can also be used in gene therapy, to make  
diagnostic probes and to express normal BRCA1 polypeptide (see AAW26522)

Sequence 5711 BP; 1953 A; 1099 C; 1277 G; 1382 T; 0 U; 0 Other;

Query Match 100.0%; Score 5587.4; DB 2; Length 5711;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 5588; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGGATTTATCTGCTCTCGCGTTGAAGAGTACAAATGTCATTAATGCTATGAGAAA 60  
Db 120 ATGGATTTATCTGCTCTCGCGTTGAAGAGTACAAATGTCATTAATGCTATGAGAAA 179  
QY 61 ATCTTAGAGTGTCCCATCTGCTGAGTTGATCAAGGAACTGTCTCCACAAGTGTGAC 120  
Db 180 ATCTTAGAGTGTCCCATCTGCTGAGTTGATCAAGGAACTGTCTCCACAAGTGTGAC 239  
QY 121 CACATATTTTGCAAAATTTTGGCATGCTGAACTTCTCAACAGAGAAAGGGCTTCCACAG 180  
Db 240 CACATATTTTGCAAAATTTTGGCATGCTGAACTTCTCAACAGAGAAAGGGCTTCCACAG 299  
QY 181 TGTCTTTTATGTAGATGATATATACCAAGAGGCTTACAGAGAAAGTACGAGATTAGT 240



Db 300 TGTCTTTAATGTAAGATGATATAACCAAAAGGAGGCTACAAGAAAGTACGAGATTAGT 359  
Qy |||||  
Db 241 CAACCTGTTGAAGAGCTATTGAAAATCAATTTGTGCTTTTCAGCTTGACACAGGTTGGAG 300  
Qy |||||  
Db 360 CAACCTGTTGAAGAGCTATTGAAAATCAATTTGTGCTTTTCAGCTTGACACAGGTTGGAG 419  
Qy |||||  
Db 301 TATGCAAAACAGCTATTAATTTGCAAAAAGGAAAATAACTCTCTGAAACATCTAAAGAT 360  
Qy |||||  
Db 420 TATGCAAAACAGCTATTAATTTGCAAAAAGGAAAATAACTCTCTGAAACATCTAAAGAT 479  
Qy |||||  
Db 361 GAATGTTCTATCATCCAAAGTATGGGCTACAGAAAACGTCGCCAAAAGAGCTTCTACAGAT 420  
Qy |||||  
Db 480 GAAGTTTCTATCATCCAAAGTATGGGCTACAGAAAACGTCGCCAAAAGAGCTTCTACAGAT 539  
Qy |||||  
Db 421 GAACCCGAAATCTCTCTGAGGAAACAGTCTCAGTGTCCAACTCTCTACACTTGA 480  
Qy |||||  
Db 540 GAACCCGAAATCTCTCTGAGGAAACAGTCTCAGTGTCCAACTCTCTACACTTGA 599  
Qy |||||  
Db 481 ACTGTGAGAACTCTGAGGCAAAAGCAGCGGATACAACCTCAAAGAGCGTCTGTCTACAT 540  
Qy |||||  
Db 600 ACTGTGAGAACTCTGAGGCAAAAGCAGCGGATACAACCTCAAAGAGCGTCTGTCTACAT 659  
Qy |||||  
Db 541 GAATGCGATCTGATCTCTCTGAGGAAACAGTCTCAGTGTCCAACTCTCTACACTTGA 600  
Qy |||||  
Db 660 GAATGCGATCTGATCTCTCTGAGGAAACAGTCTCAGTGTCCAACTCTCTACACTTGA 719  
Qy |||||  
Qy 601 GATCAAGAAATGTTTCAAAATCACCCCTCAAGGAAACAGGAGTGAATCAGTTGGATCT 660  
Qy |||||  
Db 720 GATCAAGAAATGTTTCAAAATCACCCCTCAAGGAAACAGGAGTGAATCAGTTGGATCT 779  
Qy |||||  
Qy 561 GCAAAAAGGCTGCTGTGAAATTTCTGAGACGGATGTAACTAAATCTGAACATCATCAA 720  
Qy |||||  
Db 780 GCAAAAAGGCTGCTGTGAAATTTCTGAGACGGATGTAACTAAATCTGAACATCATCAA 839  
Qy |||||  
Db 721 CCCAGTAATTAATGATTTGAACACCACTGAGGAGCGTGCAGCTGAGGGCAATCAGAAAAG 780  
Qy |||||  
Db 840 CCCAGTAATTAATGATTTGAACACCACTGAGGAGCGTGCAGCTGAGGGCAATCAGAAAAG 899  
Qy |||||  
Qy 781 TATCAGGGTATGCTGTTTCAAACTGCTGAGGACCAATGTCGCAAAATCTCATGCC 840  
Qy |||||  
Db 900 TATCAGGGTATGCTGTTTCAAACTGCTGAGGACCAATGTCGCAAAATCTCATGCC 959  
Qy |||||  
Qy 841 AGCTCATACAGATGAGACAGCAGTTTATTTACTCACTAAAGACAGATGATGTAGAA 900  
Qy |||||  
Db 960 AGCTCATACAGATGAGACAGCAGTTTATTTACTCACTAAAGACAGATGATGTAGAA 1019  
Qy |||||  
Qy 901 AAGGCTGAATTTCTGTAATAAAGCAACAGCCTGGCTTAGCAAGGAGCCCAACATACAGA 960  
Qy |||||  
Db 1020 AAGGCTGAATTTCTGTAATAAAGCAACAGCCTGGCTTAGCAAGGAGCCCAACATACAGA 1079  
Qy |||||  
Qy 961 TGGGCTGGAATGAAGAACATGTAATGATAGGAGGAGTCCAGCAAGAAAAGGTA 1020  
Qy |||||  
Db 1080 TGGGCTGGAATGAAGAACATGTAATGATAGGAGGAGTCCAGCAAGAAAAGGTA 1139  
Qy |||||  
Qy 1021 GATCTGAATGCTGATCCCTGTGTGAGAGAAAAGAAATGGAATAGCAGAACTGCCATGC 1080  
Qy |||||  
Db 1140 GATCTGAATGCTGATCCCTGTGTGAGAGAAAAGAAATGGAATAGCAGAACTGCCATGC 1199  
Qy |||||  
Qy 1081 TCAGAGAACTCTAGAGTACTGAAGATGTTCTCTTGATTAACACTAAATAGCAGCATTCAG 1140  
Qy |||||  
Db 1200 TCAGAGAACTCTAGAGTACTGAAGATGTTCTCTTGATTAACACTAAATAGCAGCATTCAG 1259  
Qy |||||  
Qy 1141 AAAGTTAAAGTGGTGTCTCAGAAAGTGAATGTTAGTGTCTGATGACTCAGCATGAT 1200  
Qy |||||  
Db 1260 AAAGTTAAAGTGGTGTCTCAGAAAGTGAATGTTAGTGTCTGATGACTCAGCATGAT 1319  
Qy |||||  
Qy 1201 GGGGAGTCTGAATCAAAATGCCAAAGTACTGATGTATTTGACGCTTCAATAGAGGTAGAT 1260  
Qy |||||  
Db 1320 GGGGAGTCTGAATCAAAATGCCAAAGTACTGATGTATTTGACGCTTCAATAGAGGTAGAT 1379  
Qy |||||  
Qy 1261 GAATATTTCTGGTCTTCAGAGAAAATAGACTTTACTGSCCAGTCACTCATGAGGCTTTA 1320  
Qy |||||

Db 1380 GAATATTTCTGGTCTCTTCAGAGAAAATAGACTTTACTGGCCAGTGATCTCTCATGAGGCTTTA 1439  
Qy |||||  
Db 1321 ATATGTAAAGTGAAGAGTTCACCTCCAAATCAGTAGAGAGTAATATTGAAGACAAAATA 1380  
Qy |||||  
Db 1440 ATATGTAAAGTGAAGAGTTCACCTCCAAATCAGTAGAGAGTAATATTGAAGACAAAATA 1499  
Qy |||||  
Db 1381 TTTTGGAAAACTTATCGGAAGAAAGCAAGCCCTCCCAACTTAAGCCATGTAACTGAAAAT 1440  
Qy |||||  
Db 1500 TTTTGGAAAACTTATCGGAAGAAAGCAAGCCCTCCCAACTTAAGCCATGTAACTGAAAAT 1559  
Qy |||||  
Qy 1441 CTAAATTAAGAGCAATTTGTTACTGAGCCACAGATAATAACAAGAGGTCCTCCCTCAAAAT 1500  
Qy |||||  
Db 1560 CTAAATTAAGAGCAATTTGTTACTGAGCCACAGATAATAACAAGAGGTCCTCCCTCAAAAT 1619  
Qy |||||  
Qy 1501 AAATTAAGCGTAAAGAGAGCACTACATCAGGCGCTTCACTCTGAGGATTTTATCAAGAAA 1560  
Qy |||||  
Db 1620 AAATTAAGCGTAAAGAGAGCACTACATCAGGCGCTTCACTCTGAGGATTTTATCAAGAAA 1679  
Qy |||||  
Qy 1561 GCAGATTTGGCAGTTCAAAAGACTCTCTGAAATGATAAATCAGGGAACTAAACCAACGGAG 1620  
Qy |||||  
Db 1680 GCAGATTTGGCAGTTCAAAAGACTCTCTGAAATGATAAATCAGGGAACTAAACCAACGGAG 1739  
Qy |||||  
Qy 1621 CAGAAATGGTCAAGTGAATTAATTAATAGTGGTCAAGAGATAAAGGAGGAGT 1680  
Qy |||||  
Db 1740 CAGAAATGGTCAAGTGAATTAATTAATAGTGGTCAAGAGATAAAGGAGGAGT 1799  
Qy |||||  
Qy 1681 TCTATTCAGAAATGAGAAAAATCCTAAACCAATAGAAATCACTCGAAAAAGAAATCTGCTTC 1740  
Qy |||||  
Db 1800 TCTATTCAGAAATGAGAAAAATCCTAAACCAATAGAAATCACTCGAAAAAGAAATCTGCTTC 1859  
Qy |||||  
Qy 1741 AAAACGAAGCTGAACCTTATAGCAGCAGTATAGCCAAATATGAACTCGAAATTAATATC 1800  
Qy |||||  
Db 1860 AAAACGAAGCTGAACCTTATAGCAGCAGTATAGCCAAATATGAACTCGAAATTAATATC 1919  
Qy |||||  
Qy 1801 CACAAATCAAAAGCACTTAAAGAAATAGGCTGAGGAGGAGTCTTCTACAGGAGTAT 1860  
Qy |||||  
Db 1920 CACAAATCAAAAGCACTTAAAGAAATAGGCTGAGGAGGAGTCTTCTACAGGAGTAT 1979  
Qy |||||  
Qy 1861 CATGGCTTGAATCTAGTAGTCAGTAGAAATCTAAGCCCACTTAATTTGATGAAATGCAA 1920  
Qy |||||  
Db 1980 CATGGCTTGAATCTAGTAGTCAGTAGAAATCTAAGCCCACTTAATTTGATGAAATGCAA 2039  
Qy |||||  
Qy 1921 ATTGATAGTGTCTTAGCAGTGAAGAGATAAAGAAAAAAGTACAACCAATGCCAGTTC 1980  
Qy |||||  
Db 2040 ATTGATAGTGTCTTAGCAGTGAAGAGATAAAGAAAAAAGTACAACCAATGCCAGTTC 2099  
Qy |||||  
Qy 1981 AGGCAAGCAGAGAAACCTACAACTATGGAAGGTAAAGAACCTGCAACTGGAAGCAAGAG 2040  
Qy |||||  
Db 2100 AGGCAAGCAGAGAAACCTACAACTATGGAAGGTAAAGAACCTGCAACTGGAAGCAAGAG 2159  
Qy |||||  
Qy 2041 AGTAACAGCCCAATGAAAGACAGTAAAGACATGACAGTGTACTTTCCAGAGCTG 2100  
Qy |||||  
Db 2160 AGTAACAGCCCAATGAAAGACAGTAAAGACATGACAGTGTACTTTCCAGAGCTG 2219  
Qy |||||  
Qy 2101 AAGTTAAACAAATGCACTGTTCTTTTACTAAGTGTTCAAATACCAAGTGAATTAAGAAA 2160  
Qy |||||  
Db 2220 AAGTTAAACAAATGCACTGTTCTTTTACTAAGTGTTCAAATACCAAGTGAATTAAGAAA 2279  
Qy |||||  
Qy 2161 TTTGTCAATCTCTAGCTTCCAAAGAGAGAAAGAAAGAAAGAAAGTAAAGTAAAGT 2220  
Qy |||||  
Db 2280 TTTGTCAATCTCTAGCTTCCAAAGAGAGAAAGAAAGAAAGAAAGTAAAGTAAAGT 2339  
Qy |||||  
Qy 2221 TCTAAATATGCTGAAGAGACCCCAAGATCTCATGTTAAGTGAAGAGGGTGTTCGAAACT 2280  
Qy |||||  
Db 2340 TCTAAATATGCTGAAGAGACCCCAAGATCTCATGTTAAGTGAAGAGGGTGTTCGAAACT 2399  
Qy |||||  
Qy 2281 GAAAGATCTGTAGAGATGAGTATTTCACTGGTACTCTGGTACTGATTTATGGCACTCAG 2340  
Qy |||||  
Db 2400 GAAAGATCTGTAGAGATGAGTATTTCACTGGTACTCTGGTACTGATTTATGGCACTCAG 2459  
Qy |||||  
Qy 2341 GAAAGTATCTGTTACTGGAAGTGTAGCACTCTTAGGGAAGGCAAGAAACAGAAACCAATAAA 2400  
Qy |||||  
Db 2460 GAAAGTATCTGTTACTGGAAGTGTAGCACTCTTAGGGAAGGCAAGAAACAGAAACCAATAAA 2519  
Qy |||||



4680 AACCTACCATCTCAAGAGGCTCAITTAAGGTGTGATGTGAGGAGCAACAGCTGGAA 4739  
4621 GAGTCTGGCCACACAGATTTGACCGAACAATCTTACTTGGCCAGGCAAGATCTAGAGGA 4680  
4740 GAGTCTGGCCACACAGATTTGACCGAACAATCTTACTTGGCCAGGCAAGATCTAGAGGA 4799  
4681 ACCCTTTACCTGGAATCTGGAATCAGGCTCTTCTCTGATGACCCCTGAATCTGATCTCTCT 4740  
4800 ACCCTTTACCTGGAATCTGGAATCAGGCTCTTCTCTGATGACCCCTGAATCTGATCTCTCT 4859  
4741 GAAGACAGAGCCACAGATGAGCTGCTGTTGGCAACATACATCTTCAACTCTGCAATG 4800  
4860 GAAGACAGAGCCACAGATGAGCTGCTGTTGGCAACATACATCTTCAACTCTGCAATG 4919  
4801 AAAGTTCCTCCAAATTTGAAGTTGCAAGATCTGCCAGAGGTCAGCTGCTGCTCATCTACT 4860  
4920 AAAGTTCCTCCAAATTTGAAGTTGCAAGATCTGCCAGAGGTCAGCTGCTGCTCATCTACT 4979  
4861 GATCTCTGGGTATTAATGCAATGGAAGAAAGTGTGAGCGAGGAGAAAGCAAGATTGACA 4920  
4980 GATCTCTGGGTATTAATGCAATGGAAGAAAGTGTGAGCGAGGAGAAAGCAAGATTGACA 5039  
4921 GCTTCAACAGAGAGGCTCAACAAAGAAATGTCATGCTGCTGCTGCCCTGACCCAGAA 4980  
5040 GCTTCAACAGAGAGGCTCAACAAAGAAATGTCATGCTGCTGCTGCCCTGACCCAGAA 5099  
4981 GAATTTATGCTGCTGTAACAAGTTTGGCCAGAAACACACATCACTTTAACTTAATTT 5040  
5100 GAATTTATGCTGCTGTAACAAGTTTGGCCAGAAACACACATCACTTTAACTTAATTT 5159  
5041 ACTCAAGAGACTACTCATGTTGTTATGAAGAAACAGATCTGAGTTGTTGTTGAGCAGCA 5100  
5160 ACTCAAGAGACTACTCATGTTGTTATGAAGAAACAGATCTGAGTTGTTGTTGAGCAGCA 5219  
5101 CTGAATATTTCTAGGAATTCGGGAGGAAATGGGTAGTAGTATTTCTGGGTGACC 5160  
5220 CTGAATATTTCTAGGAATTCGGGAGGAAATGGGTAGTAGTATTTCTGGGTGACC 5279  
5161 CAGTCTATTAAGAAAGAAATGCTGAATGAGATGATTTGAGTTCAGAGGAGATGTC 5220  
5280 CAGTCTATTAAGAAAGAAATGCTGAATGAGATGATTTGAGTTCAGAGGAGATGTC 5339  
5221 GTCAATGGAAGAAACCAAGGTCACAAAGGAGCAAGAGATCCCAAGGACAGAAAGATC 5280  
5340 GTCAATGGAAGAAACCAAGGTCACAAAGGAGCAAGAGATCCCAAGGACAGAAAGATC 5399  
5281 TTCAAGGGGCTAGAAATCTGTTGCTATGGGCTTACCAACATGCCCAGATCAACTG 5340  
5400 TTCAAGGGGCTAGAAATCTGTTGCTATGGGCTTACCAACATGCCCAGATCAACTG 5459  
5341 GAATGATGCTACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5400  
5460 GAATGATGCTACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5519  
5401 GGCAAGGTGTCCACCCCAATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 5460  
5520 GGCAAGGTGTCCACCCCAATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 5579  
5461 TTCCATGCAATTTGGGCAAGATGTTGAGGCACTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 5520  
5580 TTCCATGCAATTTGGGCAAGATGTTGAGGCACTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 5639  
5521 AGTGTAGCTCTTACCAAGTCCAGGAGCTGGACACTTACCTGATACCCAGATCCCCAC 5580  
5640 AGTGTAGCTCTTACCAAGTCCAGGAGCTGGACACTTACCTGATACCCAGATCCCCAC 5699  
5581 AGCCTACTAC 5589  
5700 AGCCTACTAC 5708

RESULT 14

AAV46448  
ID AAV46448 standard; cDNA; 5711 BP.  
XX  
AC AAV46448;  
XX  
DT 18-NOV-1998 (first entry)  
XX  
DE Human BRCA1 omil cDNA.  
XX  
KW BRCA1; omil; human; breast and ovarian cancer predisposing gene;  
XX polymorphism; susceptibility; anti-oncogene; tumour suppressor;  
XX chromosome 17q; ss.  
XX  
OS Homo sapiens.  
XX  
FH Location/Qualifiers  
FT 120..5711  
CDS /\*tag= a  
FT /product= "BRCA1 omil protein"  
XX  
XX US5750400-A.  
XX  
XX 12-MAY-1998.  
XX  
XX 12-FEB-1997; 97US-00798691.  
XX  
XX 12-FEB-1996; 96US-00598591.  
XX  
XX (ONCO-) ONCORMED INC.  
XX  
XX Olson SJ, Murphy PD, Zeng B, Alvares CP, Schelter DB, Allen AC;  
XX Critz BS;  
XX  
XX WPI; 1998-296774/26.  
XX P-PSDB; AAN76098.  
XX  
XX BRCA1 omil gene coding sequences - useful for distinguishing between  
XX polymorphisms and mutation(s) in the screening for disposition to breast  
XX or ovarian cancer.  
XX  
XX Claim 2d; Col 27-32; 54pp; English.  
XX  
XX This sequence encodes the human BRCA1 (breast and ovarian cancer  
XX predisposing gene) omil gene. This sequence and polymorphic variations of  
XX this sequence are useful for the identification of an individual who may  
XX or may not have an increased susceptibility to breast or ovarian cancer.  
XX The sequences used identify gene changes which are due to polymorphisms,  
XX rather than cancer causing mutations. BRCA1 is an anti-oncogene (tumour  
XX suppressor) which is involved in genetic inheritance of cancers,  
XX especially breast and ovarian cancer. It is found at human chromosome 17q  
XX which is known to be linked to cancer susceptibility, especially breast  
XX cancer. Cells containing a mutation in this gene lose the wild-type  
XX function of BRCA1 and are more susceptible to cancers  
XX  
XX Sequence 5711 BP; 1953 A; 1099 C; 1277 G; 1382 T; 0 U; 0 Other;  
XX

Query Match 100.0%; Score 5587.4; DB 2; Length 5711;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 5588; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATCGATTATCTGCTTCGCGCTTGAAGAGTACAAATGTCATTAATGCTATGCGAGAA 60  
DB 120 ATGGAATTTATCTGCTTCGCGCTTGAAGAGTACAAATGTCATTAATGCTATGCGAGAA 179  
QY 61 ATCTTAGAGTGTCCCATCTGCTGGAAGTGTGATCAAGAAACCTGTCTCCCAAGTGTGAC 120  
DB 180 ATCTTAGAGTGTCCCATCTGCTGGAAGTGTGATCAAGAAACCTGTCTCCCAAGTGTGAC 239  
QY 121 CACATATTTTGCATAATTTTGCATGCTGAACACTTCTCAACAGAGAAAGGCTTCCACAG 180  
DB 240 CACATATTTTGCATAATTTTGCATGCTGAACACTTCTCAACAGAGAAAGGCTTCCACAG 299  
QY 181 TGTCTTTATGTAAGAATGATATATAACCAAAAGAGCGCTACAAGAAAGTACGAGATTTAGT 240

|||||  
300 TGTCTTTATGTAGATGATATATACCAAAAGAGCCCTACAGAAGTACAGATTTAGT 359  
241 CAACCTGTGTAGAGCTATTTGAAATCATTTTGTCTTTTCAGCTTGTACACAGGTTTGGAG 300  
360 CAACCTGTGTAGAGCTATTTGAAATCATTTTGTCTTTTCAGCTTGTACACAGGTTTGGAG 419  
301 TATCGAACACGCTATATTTTGC AAAAGGAAATTAACCTCTCTGACACATCTTAARAGAT 360  
420 TATGCAAAACGCTATATTTTGC AAAAGGAAATTAACCTCTCTGACACATCTTAARAGAT 479  
361 GAAGTTTCTATCATCTCAAAAGTATGGCTACAGAAACCGTGCCAAAAGACCTTCTACAGAGT 420  
480 GAAGTTTCTATCATCTCAAAAGTATGGCTACAGAAACCGTGCCAAAAGACCTTCTACAGAGT 539  
421 GAAACCGGAAATCTCTCTGAGGAAACAGCTCTCAGTGTCCAACTCTCTAACTTTGGA 480  
540 GAAACCGGAAATCTCTCTGAGGAAACAGCTCTCAGTGTCCAACTCTCTAACTTTGGA 599  
481 ACTGTGAGAACTCTGAGGAAACAGCTCTCAGTGTCCAACTCTCTAACTTTGGA 540  
600 ACTGTGAGAACTCTGAGGAAACAGCTCTCAGTGTCCAACTCTCTAACTTTGGA 659  
541 GAATTTGGATCTGATCTCTGAGGAAACAGCTCTCAGTGTCCAACTCTCTAACTTTGGA 600  
660 GAATTTGGATCTGATCTCTGAGGAAACAGCTCTCAGTGTCCAACTCTCTAACTTTGGA 719  
601 GATCAAGAAATTTGTAACAAATCAACCTCAAGGAAACAGCTCTCAGTGTCCAACTTTT 660  
720 GATCAAGAAATTTGTAACAAATCAACCTCAAGGAAACAGCTCTCAGTGTCCAACTTTT 779  
661 GCAAAAAGGCTGTCTGTAATTTTCTGAGGAAACAGCTCTCAGTGTCCAACTTTTCA 720  
780 GCAAAAAGGCTGTCTGTAATTTTCTGAGGAAACAGCTCTCAGTGTCCAACTTTTCA 839  
721 CCCAGTAATTAATGTTTGAACCACTCAAGGAAACAGCTCTCAGTGTCCAACTTTTCA 780  
840 CCCAGTAATTAATGTTTGAACCACTCAAGGAAACAGCTCTCAGTGTCCAACTTTTCA 899  
781 TATCAGGATAGTCTGTTTCAAACTTGCATGTGAGGAAACAGCTCTCAGTGTCCAACTTT 840  
900 TATCAGGATAGTCTGTTTCAAACTTGCATGTGAGGAAACAGCTCTCAGTGTCCAACTTT 959  
841 AGCTCATTAAGGATAGGAAACAGCTCTGTAATTTTCTCAGTGTGAGGAAACAGCTTTAG 900  
960 AGCTCATTAAGGATAGGAAACAGCTCTGTAATTTTCTCAGTGTGAGGAAACAGCTTTAG 1019  
901 AAGGCTGAAATTTCTGTAATTAAGGAAACAGCTCTGTAATTTTCTCAGTGTGAGGAA 960  
1020 AAGGCTGAAATTTCTGTAATTAAGGAAACAGCTCTGTAATTTTCTCAGTGTGAGGAA 1079  
961 TGGGCTGGAAGTAAAGGAAACAGCTCTGTAATTTTCTCAGTGTGAGGAAACAGCTTTAG 1020  
1080 TGGGCTGGAAGTAAAGGAAACAGCTCTGTAATTTTCTCAGTGTGAGGAAACAGCTTTAG 1139  
1021 GATCTGAATCTGATCCCTGTTGAGGAAACAGCTCTGTAATTTTCTCAGTGTGAGGAA 1080  
1140 GATCTGAATCTGATCCCTGTTGAGGAAACAGCTCTGTAATTTTCTCAGTGTGAGGAA 1199  
1081 TCAGAGAACTCTGAGGAAACAGCTCTGTAATTTTCTCAGTGTGAGGAAACAGCTTTAG 1140  
1200 TCAGAGAACTCTGAGGAAACAGCTCTGTAATTTTCTCAGTGTGAGGAAACAGCTTTAG 1259  
1141 AAAGTTAATGATGTTTTCAGAGGAAACAGCTCTGTAATTTTCTCAGTGTGAGGAAAC 1200  
1260 AAAGTTAATGATGTTTTCAGAGGAAACAGCTCTGTAATTTTCTCAGTGTGAGGAAAC 1319  
1201 GGGAGTCTGAATCAAAATGCAAGTATGATGTTTTCAGAGGAAACAGCTTTAGAGGTTAG 1260  
1320 GGGAGTCTGAATCAAAATGCAAGTATGATGTTTTCAGAGGAAACAGCTTTAGAGGTTAG 1379  
1261 GAATATCTGTTCTTCAAGGAAACAGCTCTGTAATTTTCTCAGTGTGAGGAAACAGCTTT 1320  
|||||

Db 1380 GAATATCTGTTCTTTCAGAGAAATAGACTTACTGGCCAGTGTACTCTCATGAGGCTTTA 1439  
Qy 1321 ATATGTAAAGTGAAGAGTTCTCTCAAAATCAGTGTAGAGTAATATTTGAAGCAAAATA 1380  
Db 1440 ATATGTAAAGTGAAGAGTTCTCTCAAAATCAGTGTAGAGTAATATTTGAAGCAAAATA 1499  
Qy 1381 TTTTGGAAACCTTATCGGAAAGCAAGCTCCCAACTTAAAGCCATGTAACTGAAAT 1440  
Db 1500 TTTTGGAAACCTTATCGGAAAGCAAGCTCCCAACTTAAAGCCATGTAACTGAAAT 1559  
Qy 1441 CTAATTTATAGGAGCATTTTGTACTGAGCCACAGATAATTAAGAGCGTCCCTCAAAAT 1500  
Db 1560 CTAATTTATAGGAGCATTTTGTACTGAGCCACAGATAATTAAGAGCGTCCCTCAAAAT 1619  
Qy 1501 AAATTTAAAGCGTAAAGAGAGCTCATCAGGCTTCTCTCTGAGGATTTTATCAAGAA 1560  
Db 1620 AAATTTAAAGCGTAAAGAGAGCTCATCAGGCTTCTCTCTGAGGATTTTATCAAGAA 1679  
Qy 1561 GCAGATTTGGCGATTTCAAAAGAGCTCTGAAATGATAAATCAGGAACTAAACCAACGGAG 1620  
Db 1680 GCAGATTTGGCGATTTCAAAAGAGCTCTGAAATGATAAATCAGGAACTAAACCAACGGAG 1739  
Qy 1621 CAGATTTGCTCAGTGTGATTAATTTACTTAATAGTGTCTATGAGTAATTAACCAAGTGAT 1680  
Db 1740 CAGATTTGCTCAGTGTGATTAATTTACTTAATAGTGTCTATGAGTAATTAACCAAGTGAT 1799  
Qy 1681 TCTATTTCAAGATCAGAAAAATCTTAACCAATAGAAATCACTCGAAAAAGAACTCTGCTTTC 1740  
Db 1800 TCTATTTCAAGATCAGAAAAATCTTAACCAATAGAAATCACTCGAAAAAGAACTCTGCTTTC 1859  
Qy 1741 AAACGAAAGCTGAACCTTATAGAGCAGTATAAGCAATATGGAATCTGAAATTAATATTC 1800  
Db 1860 AAACGAAAGCTGAACCTTATAGAGCAGTATAAGCAATATGGAATCTGAAATTAATATTC 1919  
Qy 1801 CACAAATTTCAAAAGCAGCTTAAAGAAATAGGCTGAGGAGAACTTCTTCTACAGGCAATTT 1860  
Db 1920 CACAAATTTCAAAAGCAGCTTAAAGAAATAGGCTGAGGAGAACTTCTTCTACAGGCAATTT 1979  
Qy 1861 CATGCTTTGAACTAGTGTCTAGTGAATTAAGCCCACTTAAGCCCACTTAAGTTGTA 1920  
Db 1980 CATGCTTTGAACTAGTGTCTAGTGAATTAAGCCCACTTAAGCCCACTTAAGTTGTA 2039  
Qy 1921 ATTGTATGTTTCTTACAGCAGTGAAGATTAAGAAAAAGAACTTACAACTGCAAGTCC 1980  
Db 2040 ATTGTATGTTTCTTACAGCAGTGAAGATTAAGAAAAAGAACTTACAACTGCAAGTCC 2099  
Qy 1981 AGGCACAGCAGAAACCTCAACTCATGGAAGTAAAGAACTTCAACTGCAAGTCCAGAGAG 2040  
Db 2100 AGGCACAGCAGAAACCTCAACTCATGGAAGTAAAGAACTTCAACTGCAAGTCCAGAGAG 2159  
Qy 2041 AGTAACAGCCCAATGAAACAGACAGTAAAGACATGACAGTGTACTTTCCAGAGCTG 2100  
Db 2160 AGTAACAGCCCAATGAAACAGACAGTAAAGACATGACAGTGTACTTTCCAGAGCTG 2219  
Qy 2101 AAGTTAAACAAATGCACTGCTGTTCTTTTACTAAGTGTTCAAATACCAGTGAACCTTAAAGAA 2160  
Db 2220 AAGTTAAACAAATGCACTGCTGTTCTTTTACTAAGTGTTCAAATACCAGTGAACCTTAAAGAA 2279  
Qy 2161 TTTTGTCAATCTCTAGGCTTCCAAAGAGAAAGAAAGAGAACTAGAAACAGTAAAGT 2220  
Db 2280 TTTTGTCAATCTCTAGGCTTCCAAAGAGAAAGAAAGAGAACTAGAAACAGTAAAGT 2339  
Qy 2221 TCTAATATGCTGAAAGACCCCAAGATCTCATGTTAAGTGGAGAAAGGTTTTCGAAACT 2280  
Db 2340 TCTAATATGCTGAAAGACCCCAAGATCTCATGTTAAGTGGAGAAAGGTTTTCGAAACT 2399  
Qy 2281 GAAAGATCTGTAGAGTAGCAGTATTTCACTGGAATCTGTTACTGTTACTGTTATGGCACTCAG 2340  
Db 2400 GAAAGATCTGTAGAGTAGCAGTATTTCACTGGAATCTGTTACTGTTACTGTTATGGCACTCAG 2459  
Qy 2341 GAAAGTATCTCTTACTGGAAGTGTAGCACTCTAGGAAAGGCAAAACAGAAACCAATAAA 2400  
Db 2460 GAAAGTATCTCTTACTGGAAGTGTAGCACTCTAGGAAAGGCAAAACAGAAACCAATAAA 2519

QY 2401 TGTGTAGTCAAGTGTGAGCAATTTGAAACCCCAAGGACTAATTCATGTTGTTCCAAA 2460  
Db 2520 TGTGTAGTCAAGTGTGAGCAATTTGAAACCCCAAGGACTAATTCATGTTGTTCCAAA 2579  
QY 2461 GATAATAGAAATGACACAGAGGCTTTAAAGTATCCATTGGGACATGAAGTTAACCAAGT 2520  
Db 2580 GATAATAGAAATGACACAGAGGCTTTAAAGTATCCATTGGGACATGAAGTTAACCAAGT 2639  
QY 2521 CGGAAACAAAGCATAGAAATGGAAGAAAGTGAATCTGATGCTCAGTATTTGCAAGATACA 2580  
Db 2640 CGGAAACAAAGCATAGAAATGGAAGAAAGTGAATCTGATGCTCAGTATTTGCAAGATACA 2699  
QY 2581 TTCAAGGTTTCAAGGCGCAGTCAATTTGCTCTGTTTCAATCCAGGAAATGCGAGAGAG 2640  
Db 2700 TTCAAGGTTTCAAGGCGCAGTCAATTTGCTCTGTTTCAATCCAGGAAATGCGAGAGAG 2759  
QY 2641 GAATGTCCAACTTCTCTGCCACTCTTGGGCTCTTAAAGAAACAAAGTCCAAAGTCACT 2700  
Db 2760 GAATGTCCAACTTCTCTGCCACTCTTGGGCTCTTAAAGAAACAAAGTCCAAAGTCACT 2819  
QY 2701 TTTGAATGTGAACAAAGGAGAAATCAAGGAAAGTGAATGCTAATATCAAGCCCTGTA 2760  
Db 2820 TTTGAATGTGAACAAAGGAGAAATCAAGGAAAGTGAATGCTAATATCAAGCCCTGTA 2879  
QY 2761 CAGACAGTTAATATCACTGAGGCTTTCTGTTGTTGCTCAGAAAGATAGCCAGTTGAT 2820  
Db 2880 CAGACAGTTAATATCACTGAGGCTTTCTGTTGTTGCTCAGAAAGATAGCCAGTTGAT 2939  
QY 2821 AATGCCAAATGTAGTATCAAGAGGCTCTAGGTTTGTCTATCACTCAGTTCAGAGGC 2880  
Db 2940 AATGCCAAATGTAGTATCAAGAGGCTCTAGGTTTGTCTATCACTCAGTTCAGAGGC 2999  
QY 2881 AACGAACTGGACTCATTACTCCAAATAAATCATGACCTTTTACAAACCATATCGTATA 2940  
Db 3000 AACGAACTGGACTCATTACTCCAAATAAATCATGACCTTTTACAAACCATATCGTATA 3059  
QY 2941 CCACCACTTTTCCATCAAGTCAATTTGTTAAACTAAATGTAAGAAAAATCTGCTAGAG 3000  
Db 3060 CCACCACTTTTCCATCAAGTCAATTTGTTAAACTAAATGTAAGAAAAATCTGCTAGAG 3119  
QY 3001 GAAAACTTTGAGAAACATTCATGTCACCTGAAAGAGAAATGGAATGGAACATTTCCA 3060  
Db 3120 GAAAACTTTGAGAAACATTCATGTCACCTGAAAGAGAAATGGAATGGAACATTTCCA 3179  
QY 3061 AGTACAGTGAACAATTTAGCCGTAATTAACATTTAGAGAAATGTTTTTAAAGAGCCAGC 3120  
Db 3180 AGTACAGTGAACAATTTAGCCGTAATTAACATTTAGAGAAATGTTTTTAAAGAGCCAGC 3239  
QY 3121 TCAAGCAATTAATGAAGTAGGTTCCAGTACTAATGAGTGGGCTCCAGTATTAATGAA 3180  
Db 3240 TCAAGCAATTAATGAAGTAGGTTCCAGTACTAATGAGTGGGCTCCAGTATTAATGAA 3299  
QY 3181 ATAGGTTCCAGTATGAACAACTTCAAGCAGAACTAGTAGAAACAGAGGCGCAAAATTTG 3240  
Db 3300 ATAGGTTCCAGTATGAACAACTTCAAGCAGAACTAGTAGAAACAGAGGCGCAAAATTTG 3359  
QY 3241 AATGCTATGCTTAGATTAGGGTTTGGCAACCTGAGGTCATTAACAAAGTCTTCTCGGA 3300  
Db 3360 AATGCTATGCTTAGATTAGGGTTTGGCAACCTGAGGTCATTAACAAAGTCTTCTCGGA 3419  
QY 3301 AGTAAATGTAAGCATCTCTGAAATATAAAGCAAGAAATATGAAGAGTAGTTTCAAGCTGTT 3360  
Db 3420 AGTAAATGTAAGCATCTCTGAAATATAAAGCAAGAAATATGAAGAGTAGTTTCAAGCTGTT 3479  
QY 3361 AATACAGATTTCTCTCAATCTGATTTTCAGATTAACCTTAGAAACAGCTATGGGAAGTACT 3420  
Db 3480 AATACAGATTTCTCTCAATCTGATTTTCAGATTAACCTTAGAAACAGCTATGGGAAGTACT 3539  
QY 3421 CATGCATCTCAGGTTTGTCTGAGACACCTGATGACCTGTTAGATGATGCTGAATAGAG 3480  
Db 3540 CATGCATCTCAGGTTTGTCTGAGACACCTGATGACCTGTTAGATGATGCTGAATAGAG 3599

QY 3481 GAAGATACATAGTTTTCTGATAAATGACATTAAGAAAGTTTCTGCTGTTTTTACAAAAGC 3540  
Db 3600 GAAGATACATAGTTTTCTGATAAATGACATTAAGAAAGTTTCTGCTGTTTTTACAAAAGC 3659  
QY 3541 GTCCAGAGAGGAGGCTTACAGAGGCTTCTAGCCCTTTTACCCATACACATTTGGCTCAG 3600  
Db 3660 GTCCAGAGAGGAGGCTTACAGAGGCTTCTAGCCCTTTTACCCATACACATTTGGCTCAG 3719  
QY 3601 GGTTCACGAAGAGGGGCCAAGAAATTAGAGTCTCTCAGAAGAGAACTTATCTAGTAGGAT 3660  
Db 3720 GGTTCACGAAGAGGGGCCAAGAAATTAGAGTCTCTCAGAAGAGAACTTATCTAGTAGGAT 3779  
QY 3661 GAAGAGCTTCCCTGCTTCCAAACACTGTTTATTTGTAAGTAAACAATATACCTCTCAG 3720  
Db 3780 GAAGAGCTTCCCTGCTTCCAAACACTGTTTATTTGTAAGTAAACAATATACCTCTCAG 3839  
QY 3721 TCTATAGGCATAGCACCGTGTCTACCGAGTGTCTCTCTAAGAACACAGAGGAGAAATTTA 3780  
Db 3840 TCTATAGGCATAGCACCGTGTCTACCGAGTGTCTCTCTAAGAACACAGAGGAGAAATTTA 3899  
QY 3781 TTATCATTTGAAATAGCTTAAATGACTGCTACACAGGTAATATTTGGCAAGGCACTCT 3840  
Db 3900 TTATCATTTGAAATAGCTTAAATGACTGCTACACAGGTAATATTTGGCAAGGCACTCT 3959  
QY 3841 CAGGAAACATCACCCTTAGTGAGGAAACAAAATGTTCTGTAGCTTGTGTTTCTTCAAGTGC 3900  
Db 3960 CAGGAAACATCACCCTTAGTGAGGAAACAAAATGTTCTGTAGCTTGTGTTTCTTCAAGTGC 4019  
QY 3901 AGTGAATTTGAAAGACTTGTGCAATATACAAACACCCAGGATCTTTTCTTGTGTTCT 3960  
Db 4020 AGTGAATTTGAAAGACTTGTGCAATATACAAACACCCAGGATCTTTTCTTGTGTTCT 4079  
QY 3961 TCCAAACAAATGAGGCACTCAGTCTGAAAGCAGGAGTTGGTCTGAGTGACAGGAAATTTG 4020  
Db 4080 TCCAAACAAATGAGGCACTCAGTCTGAAAGCAGGAGTTGGTCTGAGTGACAGGAAATTTG 4139  
QY 4021 GTTTCAGATGATGAAGAAAGAGAAACGGGCTTTGGAAGAAATAATCAAGAGGCAAGC 4080  
Db 4140 GTTTCAGATGATGAAGAAAGAGAAACGGGCTTTGGAAGAAATAATCAAGAGGCAAGC 4199  
QY 4081 ATGGATTCAAACTTAGTGAAGCAGCATCTGGGCTGTGAGTGAAACAGCGTCTCTGAA 4140  
Db 4200 ATGGATTCAAACTTAGTGAAGCAGCATCTGGGCTGTGAGTGAAACAGCGTCTCTGAA 4259  
QY 4141 GACTGCTCAGGCTATTCCTCTCAGAGTGACATTTTAAACACTCAGCAGAGGATACCATG 4200  
Db 4260 GACTGCTCAGGCTATTCCTCTCAGAGTGACATTTTAAACACTCAGCAGAGGATACCATG 4319  
QY 4201 CAACATACCTCATTAAGCTCCAGCAGGAAATGGGCTGAACAGCTGTGTTTAGAACAG 4260  
Db 4320 CAACATACCTCATTAAGCTCCAGCAGGAAATGGGCTGAACAGCTGTGTTTAGAACAG 4379  
QY 4261 CATGGAGCCAGCTTCTTAACAGCTACCTCTCCATCATTAAGTGACCTTTCGCCCTTGAG 4320  
Db 4380 CATGGAGCCAGCTTCTTAACAGCTACCTCTCCATCATTAAGTGACCTTTCGCCCTTGAG 4439  
QY 4321 GACTGCGGAATTCAGAAACAAAGCAGCATCAGAAAAGCAGTATTAATCTTACAGAAAGT 4380  
Db 4440 GACTGCGGAATTCAGAAACAAAGCAGCATCAGAAAAGCAGTATTAATCTTACAGAAAGT 4499  
QY 4381 AGTGAATACCTTATTAAGCCAGAAATCCAGAGGCTTTCTGCTGACAAAGTTTTCAGGTTCT 4440  
Db 4500 AGTGAATACCTTATTAAGCCAGAAATCCAGAGGCTTTCTGCTGACAAAGTTTTCAGGTTCT 4559  
QY 4441 GCAGATAGTTCTTACAGTAAAAATAAGAAACAGAGGTTGGAAGTCAATCCCTTCTAAA 4500  
Db 4560 GCAGATAGTTCTTACAGTAAAAATAAGAAACAGAGGTTGGAAGTCAATCCCTTCTAAA 4619  
QY 4501 TCCCACTCATTAGATGATAGTGGTACATGACAGTCTGCTCTGGGAGTCTTTCAGATAGA 4560  
Db 4620 TCCCACTCATTAGATGATAGTGGTACATGACAGTCTGCTCTGGGAGTCTTTCAGATAGA 4679  
QY 4561 AACTACCCATCTCAAGAGGAGCTCATTAAGGTTGTTGATGTGGAGGAGCAACAGCTGGAA 4620

Db	4680		AACTACCCATCTCAAGAGGAGCTCATTAAGGTGTGTTGATGTGGAGGAGCAACAGCTGGAA	4739
Qy	4621	GAGTCTGGGCCACACGATTTTGACGGAAACATCTTACTTTGCGCAAGCGAGAGTCTAGAGGGA	4680	
Db	4740	GAGTCTGGGCCACACGATTTTGACGGAAACATCTTACTTTGCGCAAGCGAGATCTAGAGGGA	4799	
Qy	4681	ACCCCTTACCTGGGAATCTGGGAATCAGCTCTTCTCTGATGACCTGGAATCTGATCTCTCT	4740	
Db	4800	ACCCCTTACCTGGGAATCTGGGAATCAGCTCTTCTCTGATGACCTGGAATCTGATCTCTCT	4859	
Qy	4741	GAAGACAGAGCGCCACAGAGTCAGCTCTGTGTGGCGAAACATACCATCTTCAAACCTCTGCAATTG	4800	
Db	4860	GAAGACAGAGCGCCACAGAGTCAGCTCTGTGTGGCGAAACATACCATCTTCAAACCTCTGCAATTG	4919	
Qy	4801	AAAGTTTCCCAATTTGAAAGTTGCAGAAATCTGCGCCAGAGGTCCAGCTGCTGCTCACTACT	4860	
Db	4920	AAAGTTTCCCAATTTGAAAGTTGCAGAAATCTGCGCCAGAGGTCCAGCTGCTGCTCACTACT	4979	
Qy	4861	GATACTGCTGGGTATATATGCAATCGGAAGAAAGTGTGAGCAGGGAGGAAGCCAGAAATTGACA	4920	
Db	4980	GATACTGCTGGGTATATATGCAATCGGAAGAAAGTGTGAGCAGGGAGGAAGCCAGAAATTGACA	5039	
Qy	4921	GCTTCAACAGAAAGGGTCAACAAAGAAATGTGCATGTGTGTGTCTGGCCTGGAACCCAGAA	4980	
Db	5040	GCTTCAACAGAAAGGGTCAACAAAGAAATGTGCATGTGTGTGTCTGGCCTGGAACCCAGAA	5099	
Qy	4981	GAAATTTATGCTGCTGTGATCAAGTTTGCAGAAAAACACACATCACTTTTAACTTAATTT	5040	
Db	5100	GAAATTTATGCTGCTGTGATCAAGTTTGCAGAAAAACACACATCACTTTTAACTTAATTT	5159	
Qy	5041	ACTGAAGAGACTACTCATGTTGTTATGAAAAACAGATCTGAGTTGTGTGTGGAACCGACA	5100	
Db	5160	ACTGAAGAGACTACTCATGTTGTTATGAAAAACAGATCTGAGTTGTGTGTGGAACCGACA	5219	
Qy	5101	CTGAAATATTTTCTAGGAATGCGGGAGGAAATGCGGTAGCTTAGCTATTTTCTGGGTGACC	5160	
Db	5220	CTGAAATATTTTCTAGGAATGCGGGAGGAAATGCGGTAGCTTAGCTATTTTCTGGGTGACC	5279	
Qy	5161	CAGTCTATTAAAGAAAGAAAAATGCTGAATGAGCATGATTTTGAAGTTCAGAGAGAGATGTG	5220	
Db	5280	CAGTCTATTAAAGAAAGAAAAATGCTGAATGAGCATGATTTTGAAGTTCAGAGAGAGATGTG	5339	
Qy	5321	GTCAATGGAAGAAACCAAGGTCTCAAGGGAGCAGAGAAATCCCAAGGCAGAAAGATC	5280	
Db	5340	GTCAATGGAAGAAACCAAGGTCTCAAGGGAGCAGAGAAATCCCAAGGCAGAAAGATC	5399	
Qy	5281	TTCAAGGGGCTAGAAATCTGTGTCTATGGGCCCTTTCACCAACATGCCCAACAGATCAACTG	5340	
Db	5400	TTCAAGGGGCTAGAAATCTGTGTCTATGGGCCCTTTCACCAACATGCCCAACAGATCAACTG	5459	
Qy	5341	GAATGGATGTGACAGCTGTGTGTGTCTTGTGTGTGAAGAGCTTTTCATCAATTCACCTT	5400	
Db	5460	GAATGGATGTGACAGCTGTGTGTGTCTTGTGTGTGAAGAGCTTTTCATCAATTCACCTT	5519	
Qy	5401	GGCACAGGTGTCCACCCAAATGTGTGTGTGTCAGCCAGATGCCCTGGACAGAGGCAATGGC	5460	
Db	5520	GGCACAGGTGTCCACCCAAATGTGTGTGTGTCAGCCAGATGCCCTGGACAGAGGCAATGGC	5579	
Qy	5461	TTCCATGTGAATTTGGGCGAGATGTGTGAGGCGACTGTGTGTGACCCGAGAGTGGGTGTGGAC	5520	
Db	5580	TTCCATGTGAATTTGGGCGAGATGTGTGAGGCGACTGTGTGTGACCCGAGAGTGGGTGTGGAC	5639	
Qy	5521	AGTGTAGCACTTACCAGTGCAGAGAGCTGGAACACCTACTGTGATACCCAGAGTCCCCAC	5580	
Db	5640	AGTGTAGCACTTACCAGTGCAGAGAGCTGGAACACCTACTGTGATACCCAGAGTCCCCAC	5699	
Qy	5581	AGCCACTAC	5589	
Db	5700	AGCCACTAC	5708	

AAV62180	
ID	AAV62180 standard; DNA; 5711 bp.
XX	
AC	AAV62180;
XX	
DT	11-FEB-1999 (first entry)
XX	
DE	BRCAL (omil) coding sequence.
XX	
KW	BRCAL; mutation detection; disease screening; multiple allele variation;
KW	breast cancer; ovarian cancer; cystic fibrosis; Li-Fraumeni syndrome;
KW	Duchenne muscular dystrophy; Becker muscular dystrophy; ss.
XX	
OS	Homo sapiens.
XX	
FH	Key
FT	CDS
FT	Location/Qualifiers
FT	120..5711
XX	/*tag= a
FN	WO9844157-A2.
XX	
PD	08-OCT-1998.
XX	
PF	26-MAR-1998; 98WO-US006002.
XX	
PR	28-MAR-1997; 97US-00825487.
XX	
PA	(ONCO-) ONCORMED INC.
XX	
PI	Murphy PD, White MB;
XX	
DR	WPI; 1998-542713/46.
DR	P-PSDB; AAW79655.
XX	
PT	Identifying variations in polynucleotide sequences - using allele
PT	specific hybridisation assay, sequence variation locating assay, and
PT	direct sequencing, in a stepwise procedure.
XX	
PS	Disclosure: Fig 1a-i; 62bp; English.



Db 240 CACATATTTGCAAAATTTGCATGCTGAAACTTCTCAACAGAGAGAGGCGCTTCACAG 299  
QY 181 TGTCTCTTATGTAGAGATGATATACCAAAAGAGGAGCCTACAGAAAGATGACGGAATTTAGT 240  
Db 300 TGTCTCTTATGTAGAGATGATATACCAAAAGAGGAGCCTACAGAAAGATGACGGAATTTAGT 359  
QY 241 CAACCTGTGGAAGAGCTATTTGAAATCATTTGTGCTTTTCAGCTTTCAGCAGAGTTTGGAG 300  
Db 360 CAACCTGTGGAAGAGCTATTTGAAATCATTTGTGCTTTTCAGCTTTCAGCAGAGTTTGGAG 419  
QY 301 TATCAAAACAGCTATTAATTTGCAAAAAGAGAAATTAACCTCTCTGAAACATCTAAAGAT 360  
Db 420 TATCAAAACAGCTATTAATTTGCAAAAAGAGAAATTAACCTCTCTGAAACATCTAAAGAT 479  
QY 361 GAAGTCTTCTATCATCCAAAGATGCGGCTACAGAAACCGTGCCAAAGACATTTCTACAGAT 420  
Db 480 GAAGTCTTCTATCATCCAAAGATGCGGCTACAGAAACCGTGCCAAAGACATTTCTACAGAT 539  
QY 421 GAACCCGAAATCTCTCTGAGGAAACAGTCTCAGTGTCCAACTCTCTAACCTTGGGA 480  
Db 540 GAACCCGAAATCTCTCTGAGGAAACAGTCTCAGTGTCCAACTCTCTAACCTTGGGA 599  
QY 481 ACTGTGAGAACTCTGAGGACAAAGCAGCGGATACAGCTCAAAAGAGCTCTGTCTACAT 540  
Db 600 ACTGTGAGAACTCTGAGGACAAAGCAGCGGATACAGCTCAAAAGAGCTCTGTCTACAT 659  
QY 541 GAATGGGATCTGATTTCTCTGAGATACCGTTTAATTAAGGCAACTTATTCAGTGTGGGA 600  
Db 660 GAATGGGATCTGATTTCTCTGAGATACCGTTTAATTAAGGCAACTTATTCAGTGTGGGA 719  
QY 601 GATCAAGATTTGTACAAATCACCCCTCAAGGACAGGAGTGAATCAAGTGTGGATTC 660  
Db 720 GATCAAGATTTGTACAAATCACCCCTCAAGGACAGGAGTGAATCAAGTGTGGATTC 779  
QY 661 GCRAAAAGGCTGCTGTGTGAATTTCTGAGACGATGAACAAATCTGAACATCATCA 720  
Db 780 GCRAAAAGGCTGCTGTGTGAATTTCTGAGAGCGATGAACAAATCTGAACATCATCA 839  
QY 721 CCCAGTAAATGATTTGAACACCACTGAGAGGCTGACCTGAGAGGATCCAGAAAG 780  
Db 840 CCCAGTAAATGATTTGAACACCACTGAGAGGCTGACCTGAGAGGATCCAGAAAG 899  
QY 781 TATCAGGCTAGTTCGTGTTTCAAACTGTCATGTGAGCCATGTGCAAAATATCTCATGCC 840  
Db 900 TATCAGGCTAGTTCGTGTTTCAAACTGTCATGTGAGCCATGTGCAAAATATCTCATGCC 959  
QY 841 AGCTCTTACAGCATGAGACAGAGTTTATTAATCACTAAAGACAGATGAATGTAGAA 900  
Db 960 AGCTCAATACAGCATGAGACAGAGTTTATTAATCACTAAAGACAGATGAATGTAGAA 1019  
QY 901 AAGGCTGAATTCGTATATAAAGCAACAGCTGGCTTAGCAAGGAGCCCAACATACAGA 960  
Db 1020 AAGGCTGAATTCGTATATAAAGCAACAGCTGGCTTAGCAAGGAGCCCAACATACAGA 1079  
QY 961 TGGGCTGGAGATGAAGAAACATGPAATGATAGGCGAATCCCGACACAGAAAAAGGTA 1020  
Db 1080 TGGGCTGGAGATGAAGAAACATGPAATGATAGGCGAATCCCGACACAGAAAAAGGTA 1139  
QY 1021 GATCTGAATCTGATCCCTGTGTGAGAGAAAGATGGAATTAAGCAAGAACTGCCATGC 1080  
Db 1140 GATCTGAATCTGATCCCTGTGTGAGAGAAAGATGGAATTAAGCAAGAACTGCCATGC 1199  
QY 1081 TCAGAGAACTCTAGAGATCTGAAGATGTTCTCTTGGATTAACACTAAATAGCAGATTCAG 1140  
Db 1200 TCAGAGAACTCTAGAGATCTGAAGATGTTCTCTTGGATTAACACTAAATAGCAGATTCAG 1259  
QY 1141 AAGGTTAATGAGTGTCTTCCAGAGCTGATGATGTTTGTAGTCTCAATGAT 1200  
Db 1260 AAGGTTAATGAGTGTCTTCCAGAGCTGATGATGTTTGTAGTCTCAATGAT 1319  
QY 1201 GGGGAGTCTGAATCAAAATGCAAGTAGCTGATGTTTGGACGCTTCTAAATGAGGTAGAT 1260

Db 1320 GGGGAGTCTGAATCAAAATGCCAAAGTAGCTGATGTTTGGACGCTTCTAAATGAGGTAGAT 1379  
QY 1261 GAATATTTCTGGTCTCTCAGAGAAATAGAGCTTACTGCCAGATGATCCTCATGAGGCTTTA 1320  
Db 1380 GAATATTTCTGGTCTCTCAGAGAAATAGAGCTTACTGCCAGATGATCCTCATGAGGCTTTA 1439  
QY 1321 ATATGTAAAAGTGAAAGAGTTTCACTCCAAATCAGTAGAGAGTAATATGGAAGCAAAATA 1380  
Db 1440 ATATGTAAAAGTGAAAGAGTTTCACTCCAAATCAGTAGAGAGTAATATGGAAGCAAAATA 1499  
QY 1381 TTTGGGAAACCTTATCGGAGAGGCAAGCCTCCCAACTTAAGCCATCTTAACCTGAAAT 1440  
Db 1500 TTTGGGAAACCTTATCGGAGAGGCAAGCCTCCCAACTTAAGCCATCTTAACCTGAAAT 1559  
QY 1441 CTAATTTATAGGAGCATTTGTGTTACTGAGCCACAGATTAATCAAGAGCGTCCCTTCACAAAT 1500  
Db 1560 CTAATTTATAGGAGCATTTGTGTTACTGAGCCACAGATTAATCAAGAGCGTCCCTTCACAAAT 1619  
QY 1501 AATTTAAAGCGTAAAGGAGACCTACATCAGGCTTTCATCTCGAGGATTTTATCAAGAAA 1560  
Db 1620 AATTTAAAGCGTAAAGGAGACCTACATCAGGCTTTCATCTCGAGGATTTTATCAAGAAA 1679  
QY 1561 GCAGATTTGGCAGTTTCAAAAGAGCTCTGAAATGATATAAATCAGGGAATCAACCAAAAGGAG 1620  
Db 1680 GCAGATTTGGCAGTTTCAAAAGAGCTCTGAAATGATATAAATCAGGGAATCAACCAAAAGGAG 1739  
QY 1621 CAGAATGGTCAAGTGAATGATTAATTAATAGTGTCTGATGAGATTAATAAACAAGGTGAT 1680  
Db 1740 CAGAATGGTCAAGTGAATGATTAATTAATAGTGTCTGATGAGATTAATAAACAAGGTGAT 1799  
QY 1681 TCTATTTCAAGATGAGAAAAATCTTAACCAATAGATTAATCACTGAAAAAGATCTGCTTTC 1740  
Db 1800 TCTATTTCAAGATGAGAAAAATCTTAACCAATAGATTAATCACTGAAAAAGATCTGCTTTC 1859  
QY 1741 AAAACGAAAGCTGAACCTTAATAGCAGCAGTATTAAGCAATATGGAATCGAATTAATAATC 1800  
Db 1860 AAAACGAAAGCTGAACCTTAATAGCAGCAGTATTAAGCAATATGGAATCGAATTAATAATC 1919  
QY 1801 CACAAATTCAAAAGCAGCTTAAGAAAGATAGCTGTGAGGAGAGCTTCTTACAGGCAATAT 1860  
Db 1920 CACAAATTCAAAAGCAGCTTAAGAAAGATAGCTGTGAGGAGAGCTTCTTACAGGCAATAT 1979  
QY 1861 CATGCGCTTGAACTAGTACTAGTAGAATCTAAGCCCACTTAATTTGACTGAAATGSCAA 1920  
Db 1980 CATGCGCTTGAACTAGTACTAGTAGAATCTAAGCCCACTTAATTTGACTGAAATGSCAA 2039  
QY 1921 ATTGATAGTTGTTCTAGCAGTGAAGGATTAAGAAAAAAGTACACCAATGCGCAGTC 1980  
Db 2040 ATTGATAGTTGTTCTAGCAGTGAAGGATTAAGAAAAAAGTACACCAATGCGCAGTC 2099  
QY 1981 AGGCACAGCAGAAAACTCAACTCATGGAAGGTAAAGAACCTTGCACTGAGGCCAAGAG 2040  
Db 2100 AGGCACAGCAGAAAACTCAACTCATGGAAGGTAAAGAACCTTGCACTGAGGCCAAGAG 2159  
QY 2041 AGTAACAAGCCAAATGAACAGACAGATAAAGACATGACAGTGTACTTTCCAGAGCTG 2100  
Db 2160 AGTAACAAGCCAAATGAACAGACAGATAAAGACATGACAGTGTACTTTCCAGAGCTG 2219  
QY 2101 AAGTTTAAACAAATGCAGCTGCTTTTCTAATAGTGTTCAAATACACAGTGAATTAAGAA 2160  
Db 2220 AAGTTTAAACAAATGCAGCTGCTTTTCTAATAGTGTTCAAATACACAGTGAATTAAGAA 2279  
QY 2161 TTTGTCAATCTTAGCCTTCCAAAGAGAGAAAAAGAGAAAACTAGAAAAAGTTAAAGTG 2220  
Db 2280 TTTGTCAATCTTAGCCTTCCAAAGAGAGAAAAAGAGAAAACTAGAAAAAGTTAAAGTG 2339  
QY 2221 TCTTAATAATGCTGAGAGCCCAAGATCTCATGTTTAAGTGGAGAGAGGCTTTTGAACCT 2280  
Db 2340 TCTTAATAATGCTGAGAGCCCAAGATCTCATGTTTAAGTGGAGAGAGGCTTTTGAACCT 2399  
QY 2281 GAAAGATCTGTAGAGATGAGCAGTATTTTCACTGTGACCTGTGACTGATGATGACTCAG 2340  
Db 2400 GAAAGATCTGTAGAGATGAGCAGTATTTTCACTGTGACCTGTGACTGATGATGACTCAG 2459

QY	2341	GAAGTATCTCGTTACTGGAAAGTTAGCACTCTAGGGAAAGGCCAAAAACAGAAACCAATAATAA	2400
DB	2460	GAAGTATCTCGTTACTGGAAAGTTAGCACTCTAGGGAAAGGCCAAAAACAGAAACCAATAATAA	2519
QY	2401	TGTGTGAGTTCAGTGTGCAGCATTTTGAAACCCCAAGGAGCAATTTCTATGGTTGTTCCTCAA	2460
DB	2520	TGTGTGAGTTCAGTGTGCAGCATTTTGAAACCCCAAGGAGCAATTTCTATGGTTGTTCCTCAA	2579
QY	2461	GATATAGAAATGACACAGAAAGGCTTTAAGTATCCATTGGGACATGAAGTTAACACCAAGT	2520
DB	2580	GATATAGAAATGACACAGAAAGGCTTTAAGTATCCATTGGGACATGAAGTTAACACCAAGT	2639
QY	2521	CGGAAAAACAGCATAGAAATTCGAGAAAGTCTGAACTTTGATGCTCAGTATTTTCAGAAATACA	2580
DB	2640	CGGAAAAACAGCATAGAAATTCGAGAAAGTCTGAACTTTGATGCTCAGTATTTTCAGAAATACA	2699
QY	2581	TTCAAGGTTTCAAGGCGCCAGTCAATTTGCTCTGTTTTCAAATCCAGGAAATTCAGAAAGAG	2640
DB	2700	TTCAAGGTTTCAAGGCGCCAGTCAATTTGCTCTGTTTTCAAATCCAGGAAATTCAGAAAGAG	2759
QY	2641	GAAATGTGCAACATTTCTCTGCCCACTCTGGGTCTTTAAGAAACAAAGTCCAAAGTCACT	2700
DB	2760	GAAATGTGCAACATTTCTCTGCCCACTCTGGGTCTTTAAGAAACAAAGTCCAAAGTCACT	2819
QY	2701	TTTGAATCTGAAACAAAAGGAAAGAAATCAAGGAAAGATGAGTCTAATATCAAGCCCTGTA	2760
DB	2820	TTTGAATCTGAAACAAAAGGAAAGAAATCAAGGAAAGATGAGTCTAATATCAAGCCCTGTA	2879
QY	2761	CAGACAGTTAATATCACTGCAAGGCTTTTCTGTGTGTTCTGAAAGATATAGCCAGTTGAT	2820
DB	2880	CAGACAGTTAATATCACTGCAAGGCTTTTCTGTGTGTTCTGAAAGATATAGCCAGTTGAT	2939
QY	2821	AATGCCAAATGTAGTATCAAAAGGAGGCTCTAGGTTTGTCTATCATCTCAGTTTCAGAGGC	2880
DB	2940	AATGCCAAATGTAGTATCAAAAGGAGGCTCTAGGTTTGTCTATCATCTCAGTTTCAGAGGC	2999
QY	2881	AACGAAATCGGACTCATTTATCCAAATAAACATGACATTTTACAAAAACCATATCGTATA	2940
DB	3000	AACGAAATCGGACTCATTTATCCAAATAAACATGACATTTTACAAAAACCATATCGTATA	3059
QY	2941	CCACCACTTTTCCCATCAGTCAATTTGTTAAACTAAATGTAGAAATCTGCTAGAG	3000
DB	3060	CCACCACTTTTCCCATCAGTCAATTTGTTAAACTAAATGTAGAAATCTGCTAGAG	3119
QY	3001	GAAACATTTTGAGGAACATTCATATCTCACCTGAAAGAGAAATGGGAAATGAGAACATTC	3060
DB	3120	GAAACATTTTGAGGAACATTCATATCTCACCTGAAAGAGAAATGGGAAATGAGAACATTC	3179
QY	3061	AGTACAGTGAACACATTTAGCCGTAATTAACATTTAGAGAAATGTTTTTAAAGAGCCAGC	3120
DB	3180	AGTACAGTGAACACATTTAGCCGTAATTAACATTTAGAGAAATGTTTTTAAAGAGCCAGC	3239
QY	3121	TCAAGCAATATTAATGAAGTAGGTTCCAGTACTAATGAAGTGGCTCCAGTATTAATGAA	3180
DB	3240	TCAAGCAATATTAATGAAGTAGGTTCCAGTACTAATGAAGTGGCTCCAGTATTAATGAA	3299
QY	3181	ATAGGTTCCAGTGATGAAAAACATTTCAAGCAGAACTAGGTTAGAAACAGAGGCCCAAAATTG	3240
DB	3300	ATAGGTTCCAGTGATGAAAAACATTTCAAGCAGAACTAGGTTAGAAACAGAGGCCCAAAATTG	3359
QY	3241	AATCCTATGCTTACATTTAGGGTTTTCCAACTGAGTCTATATAAACAAAGTCTTCTCTGGA	3300
DB	3360	AATCCTATGCTTACATTTAGGGTTTTCCAACTGAGTCTATATAAACAAAGTCTTCTCTGGA	3419
QY	3301	AGTAATTTGTAAGCATCTCGAAATATAAAAAAGCAAGATATATGAAGAGTAGTTTCAGACTGTT	3360
DB	3420	AGTAATTTGTAAGCATCTCGAAATATAAAAAAGCAAGATATATGAAGAGTAGTTTCAGACTGTT	3479
QY	3361	AATACAGATTTCTCTCCATATCTGATTTTCAGATTAACCTTAGAAACAGCCTATGGGAAAGTAGT	3420
DB	3480	AATACAGATTTCTCTCCATATCTGATTTTCAGATTAACCTTAGAAACAGCCTATGGGAAAGTAGT	3539

QY	3421	CATGCATCTCAGGTTTGTTCTGAGACACCTGATGACCTGTTAGATGATGGTGAATAAAG	3480
DB	3540	CATGCATCTCAGGTTTGTTCTGAGACACCTGATGACCTGTTAGATGATGGTGAATAAAG	3599
QY	3481	GAAGATACTAGTTTTGCTGAAATGACATTAAGGAAAGTTCTGCTGTTTACGAAAAGC	3540
DB	3600	GAAGTACTAGTTTTGCTGAAATGACATTAAGGAAAGTTCTGCTGTTTACGAAAAGC	3659
QY	3541	GTCGAGAGAGGAGGCTTTAGCAGGAGTCTAGCCCTTTCAACCATACACATTTGGCTCAG	3600
DB	3660	GTCGAGAGAGGAGGCTTTAGCAGGAGTCTAGCCCTTTCAACCATACACATTTGGCTCAG	3719
QY	3601	GTTTACCGAGAGGGGCCAAGAAATTAGAGTCTCTCAGAAGAGAACTTATCTAGTGGAGAT	3660
DB	3720	GTTTACCGAGAGGGGCCAAGAAATTAGAGTCTCTCAGAAGAGAACTTATCTAGTGGAGAT	3779
QY	3661	GAAGAGCTTCCCTGCTTCCAAACACTTGTATTATTTGGTAAAGTAAACAATATACCTTCTCAG	3720
DB	3780	GAAGAGCTTCCCTGCTTCCAAACACTTGTATTATTTGGTAAAGTAAACAATATACCTTCTCAG	3839
QY	3721	TCTACTAGGCATAGCACGGTTGCTACCGAGTGTCTCTTAAAGAACACAGAGGAGAAATTTA	3780
DB	3840	TCTACTAGGCATAGCACGGTTGCTACCGAGTGTCTCTTAAAGAACACAGAGGAGAAATTTA	3899
QY	3781	TTATCATTTGAAGATAGCTTTAAATGACTCGAGTAAACCGAGTAAATATTTGGCAAAGGCATCT	3840
DB	3900	TTATCATTTGAAGATAGCTTTAAATGACTCGAGTAAACCGAGTAAATATTTGGCAAAGGCATCT	3959
QY	3841	CAGGAACATCACTTAGTAGAGGAAAAGAAATGTTCTGTAGTGTGTTTTCTTCACAGTGC	3900
DB	3960	CAGGAACATCACTTAGTAGAGGAAAAGAAATGTTCTGTAGTGTGTTTTCTTCACAGTGC	4019
QY	3901	AGTCAATTTGGAAGACTTGACTGCAATACAAACACCCAGGATCCCTTTCTTTGATTTGTTCT	3960
DB	4020	AGTGAATTTGGAAGACTTGACTGCAATACAAACACCCAGGATCCCTTTCTTTGATTTGTTCT	4079
QY	3961	TCCAAAAGAAATGAGGCATCAGTCTGAAAGCCAGGGAGTTTGGTCTGAGTGCACAGGAATTTG	4020
DB	4080	TCCAAAAGAAATGAGGCATCAGTCTGAAAGCCAGGGAGTTTGGTCTGAGTGCACAGGAATTTG	4139
QY	4021	GTTTTCACTATGAAGAAAGAGGAAAGGGCTTGGAGGAAATAAATCAAGAGGACCAAGC	4080
DB	4140	GTTTTCACTATGAAGAAAGAGGAAAGGGCTTGGAGGAAATAAATCAAGAGGACCAAGC	4199
QY	4081	ATGGATTTCAAACCTTAGGTGAAGCAGCATCTGGGTGTGAGAGTGAACCAAGCGTCTCTGAA	4140
DB	4200	ATGGATTTCAAACCTTAGGTGAAGCAGCATCTGGGTGTGAGAGTGAACCAAGCGTCTCTGAA	4259
QY	4141	GACTGCTCAGGGCTATCTCTCTAGAGTGAATTTTAAACCACTCAGCAGAGGAGTACCAGT	4200
DB	4260	GACTGCTCAGGGCTATCTCTCTAGAGTGAATTTTAAACCACTCAGCAGAGGAGTACCAGT	4319
QY	4201	CAACATAACCTGATAAGCTCCAGCAGGAAATGGCTGAACTAGAGCTGTGTTTGAACAAG	4260
DB	4320	CAACATAACCTGATAAGCTCCAGCAGGAAATGGCTGAACTAGAGCTGTGTTTGAACAAG	4379
QY	4261	CATGGGAGCAGGCTTCTTAACAGCTACCTTCCATCATTAAGTGAATCTTCTCGCCCTTGAG	4320
DB	4380	CATGGGAGCAGGCTTCTTAACAGCTACCTTCCATCATTAAGTGAATCTTCTCGCCCTTGAG	4439
QY	4321	GACCTGGAAATCCAGAACAAAGCACATCAGAAAAAGCAGTATTAACCTTCAAGAAAAAGT	4380
DB	4440	GACCTGGAAATCCAGAACAAAGCACATCAGAAAAAGCAGTATTAACCTTCAAGAAAAAGT	4499
QY	4381	AGTGAATACCTTATAGCCAGGAATCCAGAGGCCCTTTCTGTGTGAACAAGTTTGAGGTGTCT	4440
DB	4500	AGTGAATACCTTATAGCCAGGAATCCAGAGGCCCTTTCTGTGTGAACAAGTTTGAGGTGTCT	4559
QY	4441	GCAGATAGTTCTACAGTAAATAAAGAACACAGGAGTGGAAAGCTCATCCCTTCTTAAA	4500
DB	4560	GCAGATAGTTCTACAGTAAATAAAGAACACAGGAGTGGAAAGCTCATCCCTTCTTAAA	4619
QY	4501	TGCCCATCATTAGATGATAGTGGTGAATGATGCACAGTTGCTCTGGGAGTCTTTCAGAAATAGA	4560

Db	5700	AGCCACTAC	5708
Db	4620		
Qy	4620	TGCCCCATCATTAGATGATAGGGTGGTACATGACAGTTGCTCTGGGAGTCTTCAGAAATAGA	4679
Db	4561	AACTACCCATCTCAAGAGGAGCTCAFTTAAGGTTGTTGATGTGGAGGAGCAACAGCTGGAA	4620
Qy	4561	AACTACCCATCTCAAGAGGAGCTCAFTTAAGGTTGTTGATGTGGAGGAGCAACAGCTGGAA	4739
Db	4621	GAGTCTGGGCCACACAGATTGACCGAAACATCTTACTTTGCCAAGSCAAGATCTAGAGGGA	4680
Qy	4621	GAGTCTGGGCCACACAGATTGACCGAAACATCTTACTTTGCCAAGSCAAGATCTAGAGGGA	4799
Db	4740	GAGTCTGGGCCACACAGATTGACCGAAACATCTTACTTTGCCAAGSCAAGATCTAGAGGGA	4799
Qy	4681	ACCCCTTACCTGGGAATCTGGGAATCAGCCCTCTTCTCTGATGACCCCTGGAATCTGATCCTTCT	4740
Db	4800	ACCCCTTACCTGGGAATCTGGGAATCAGCCCTCTTCTCTGATGACCCCTGGAATCTGATCCTTCT	4859
Qy	4741	GAAGACAGAGCCCGAGAGTCACTGCTGTTGGCAACATACCATCTTCAACCTCTGCAATTG	4800
Db	4860	GAAGACAGAGCCCGAGAGTCACTGCTGTTGGCAACATACCATCTTCAACCTCTGCAATTG	4919
Qy	4801	AAAGTTCCCAATTTGAAGTTGCGAATCTGCGAGGCTCCAGGCTCCAGCTGCTCATACTACT	4860
Db	4920	AAAGTTCCCAATTTGAAGTTGCGAATCTGCGAGGCTCCAGGCTCCAGCTGCTCATACTACT	4979
Qy	4861	GATACCTGCTGGGTATATGCAATGGAAGATGAGAGAAAGTGTGAGCAGGAGAGCCAGAAATTGACA	4920
Db	4980	GATACCTGCTGGGTATATGCAATGGAAGATGAGAGAAAGTGTGAGCAGGAGAGCCAGAAATTGACA	5039
Qy	4921	GCTTCAACAGAAAGGCTCAACAAAGAAATGCTCATGTGGTGTCTGGCCTGACCCACAGAA	4980
Db	5040	GCTTCAACAGAAAGGCTCAACAAAGAAATGCTCATGTGGTGTCTGGCCTGACCCACAGAA	5099
Qy	4981	GAATTTATGCTCGTGTACAGTTTCCAGAAAAACACCAATCACTTTAACTTAATCTAATT	5040
Db	5100	GAATTTATGCTCGTGTACAGTTTCCAGAAAAACACCAATCACTTTAACTTAATCTAATT	5159
Qy	5041	ACTGAAGAGACTACTCATGTTGTTATGAACACGATCTGAGTTTGTGTGACGGACA	5100
Db	5160	ACTGAAGAGACTACTCATGTTGTTATGAACACGATCTGAGTTTGTGTGACGGACA	5219
Qy	5101	CTGAAATATTTCTAGGAATTCGGGAGGAAATGGGTAGTTAGCTATTTCTGGGTGACC	5160
Db	5220	CTGAAATATTTCTAGGAATTCGGGAGGAAATGGGTAGTTAGCTATTTCTGGGTGACC	5279
Qy	5161	CAGTCTATTAAAGAAAGAAATGCTGAAATGAGCATGATTTTGAAGTCAGAGGAGATGTG	5220
Db	5280	CAGTCTATTAAAGAAAGAAATGCTGAAATGAGCATGATTTTGAAGTCAGAGGAGATGTG	5339
Qy	5221	GTCAATGGAAGAAACCAACAGGTCCAAAGCGAGCAAGAGATCCAGGACAGAAAGATC	5280
Db	5340	GTCAATGGAAGAAACCAACAGGTCCAAAGCGAGCAAGAGATCCAGGACAGAAAGATC	5399
Qy	5281	TTCAAGGGGCTAGAAATCTGTTGCTATGGGCCCTTCCACCAATGCCCCACAGATCAACTG	5340
Db	5400	TTCAAGGGGCTAGAAATCTGTTGCTATGGGCCCTTCCACCAATGCCCCACAGATCAACTG	5459
Qy	5341	GAATGGATGTTACAGCTGTGTGTTCTTCTGTGTGAAGGAGCTTTTCATCATTCACCCCTT	5400
Db	5460	GAATGGATGTTACAGCTGTGTGTTCTTCTGTGTGAAGGAGCTTTTCATCATTCACCCCTT	5519
Qy	5401	GGCAACAGGTGTCAACCCAAATTTGTTGTGAGCCAGATGCTTGGACAGAGGACAAATGTC	5460
Db	5520	GGCAACAGGTGTCAACCCAAATTTGTTGTGAGCCAGATGCTTGGACAGAGGACAAATGTC	5579
Qy	5461	TTCCATGCATTTGGGAGATGTGTGAGGACCTGTGTGTGACCCGAGAGTGGTGTGGAC	5520
Db	5580	TTCCATGCATTTGGGAGATGTGTGAGGACCTGTGTGTGACCCGAGAGTGGTGTGGAC	5639
Qy	5521	AGTGTAGCACTCTACCAAGTCCAGGAGCTGACACCTACCTGTATACCCAGATCCCCCAC	5580
Db	5640	AGTGTAGCACTCTACCAAGTCCAGGAGCTGACACCTACCTGTATACCCAGATCCCCCAC	5699
Qy	5581	AGCCACTAC	5589

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 11, 2004, 15:24:58 ; Search time 1988 Seconds  
(without alignments)  
12203.953 Million cell updates/sec

Title: US-09-734-672A-3

Perfect score: 5711

Sequence: 1 AGCTCGGTGAGACTTCTCTGG.....TCCCCACACCCACTACTGA 5711

Scoring table: IDENTITY NUC  
Gapex 10.0, Gapex 1.0

Searched: 3373663 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_29Jan04:\*  
1: Geneseq1980s:\*  
2: Geneseq1990s:\*  
3: Geneseq2000s:\*  
4: Geneseq2001as:\*  
5: Geneseq2001bs:\*  
6: Geneseq2002s:\*  
7: Geneseq2003as:\*  
8: Geneseq2003bs:\*  
9: Geneseq2003cs:\*  
10: Geneseq2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5711	100.0	5711	2	AAV46450 Human BRC
2	5711	100.0	5711	3	AAC60794 Human BRC
3	5711	100.0	5711	8	ACA61333 Human BRC
4	5711	100.0	5711	9	ADC63291 Polymorph
5	5710.6	100.0	5711	2	AAV46468 Human BRC
6	5710.6	100.0	5711	2	AAV46465 Human BRC
7	5710.6	100.0	5711	2	AAV46470 Human BRC
8	5710.6	100.0	5711	2	AAV46466 Human BRC
9	5710.6	100.0	5711	2	AAV46467 Human BRC
10	5710.6	100.0	5711	2	AAV46469 Human BRC
11	5710.6	100.0	5711	2	AAV46456 Human BRC
12	5710.6	100.0	5711	2	AAV46471 Human BRC
13	5709.4	100.0	5711	2	AAV46471 Human BRC
14	5709.4	100.0	5711	2	AAV46448 Human BRC
15	5709.4	100.0	5711	2	AAV62180 BRCAL (om
16	5709.4	100.0	5711	3	AAC60793 Human BRC
17	5709.4	100.0	5711	8	ACA61332 Human BRC
18	5709.4	100.0	5711	9	ADC63287 Consensus
19	5709	100.0	5711	2	AAV46455 Human BRC
20	5709	100.0	5711	2	AAV46451 Human BRC
21	5709	100.0	5711	2	AAV46454 Human BRC
22	5709	100.0	5711	2	AAV46457 Human BRC
23	5709	100.0	5711	2	AAV46452 Human BRC

24	5709	100.0	5711	2	AAV46453	AAV46453 Human BRC
25	5707.8	99.9	5711	7	ACD25993	ACD25993 DNA encod
26	5704.2	99.9	5711	2	AAV46459	AAV46459 Human BRC
27	5704.2	99.9	5711	2	AAV46454	AAV46454 Human BRC
28	5704.2	99.9	5711	2	AAV46452	AAV46452 Human BRC
29	5704.2	99.9	5711	2	AAV46461	AAV46461 Human BRC
30	5703	99.9	5711	2	AAV46449	AAV46449 Human BRC
31	5703	99.9	5711	3	AAC60795	AAC60795 Human BRC
32	5703	99.9	5711	8	ACA61334	ACA61334 Human BRC
33	5703	99.9	5711	2	AAV46458	AAV46458 Human BRC
34	5703	99.9	5711	2	AAV46458	AAV46458 Human BRC
35	5703	99.9	5711	2	AAV46458	AAV46458 Human BRC
36	5703	99.9	5711	2	AAV46458	AAV46458 Human BRC
37	5703	99.9	5711	2	AAV46458	AAV46458 Human BRC
38	5702.6	99.9	5711	2	AAV46458	AAV46458 Human BRC
39	5702.6	99.9	5711	2	AAV46458	AAV46458 Human BRC
40	5702.6	99.9	5711	2	AAV46458	AAV46458 Human BRC
41	5701.4	99.8	5711	7	AB223502	AB223502 Nucleotid
42	5701.4	99.8	5712	2	AAT84840	AAT84840 Human bre
43	5701.4	99.8	5712	3	AAZ87995	AAZ87995 BRCAL gen
44	5701.4	99.8	5714	2	AAT18310	AAT18310 BRCAL, br
45	5701.4	99.8	5714	2	AAT17438	AAT17438 BRCAL cod

## ALIGNMENTS

RESULT 1  
AAV46450  
ID AAV46450 standard; cDNA; 5711 BP.  
XX  
AC AAV46450;  
XX  
DT 18-NOV-1998 (first entry)  
XX  
DB Human BRCAL omi3 cDNA.  
XX  
KW BRCAL; omi3; human; breast and ovarian cancer predisposing gene;  
KW polymorphism; susceptibility; anti-oncogene; tumour suppressor;  
KW chromosome 17q; ss.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
CDS 120..5711  
FT /\*tag= a  
FT /product= "BRCAL omi3 protein"  
XX  
XX US5750400-A.  
XX  
PD 12-MAY-1998.  
PF 12-FEB-1997; 97US-00798691.  
PR 12-FEB-1996; 96US-00598591.  
PA (ONCO-) ONCORMED INC.  
PI Olson SJ, Murphy PD, Zeng B, Alvares CP, Schelter DB, Allen AC;  
PI Critz BS;  
XX  
XX WPI; 1998-296774/26.  
XX P-PSDB; AAW76100.  
XX  
XX BRCAL omi gene coding sequences - useful for distinguishing between  
XX polymorphisms and mutation(s) in the screening for disposition to breast  
XX or ovarian cancer.  
XX Claim 2e; Col 55-62; 54pp; English.  
XX  
XX This sequence encodes the human BRCAL (breast and ovarian cancer  
XX predisposing gene) omi3 gene. This sequence and polymorphic variations of  
XX this sequence are useful for the identification of an individual who may

CC or may not have an increased susceptibility to breast or ovarian cancer.  
CC The sequences used identify gene changes which are due to polymorphisms,  
CC rather than cancer causing mutations. BRCA1 is an anti-oncogene (tumour  
CC suppressor) which is involved in genetic inheritance of cancers,  
CC especially breast and ovarian cancer. It is found at human chromosome 17q  
CC which is known to be linked to cancer susceptibility, especially breast  
CC cancer. Cells containing a mutation in this gene lose the wild-type  
CC function of BRCA1 and are more susceptible to cancers  
XX  
SQ

Sequence 5711 BP; 1953 A; 1098 C; 1277 G; 1383 T; 0 U; 0 Other;

Query Match 100.0%; Score 5711; DB 2; Length 5711;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 5711; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 AGCTGCTGAGACTTCCTGGACCCCGCACAGGCTGTGGGTTTCTCAGATAACTGGGCC 60
Db |||
Qy 1 AGCTGCTGAGACTTCCTGGACCCCGCACAGGCTGTGGGTTTCTCAGATAACTGGGCC 60
Db |||
Qy 61 CTTGCGCTCAGGAGGCTTCACTCTCTCTGCTGGTAAAGTTCAATTGGAAACAGAAAGAA 120
Db |||
Qy 61 CTTGCGCTCAGGAGGCTTCACTCTCTCTGCTGGTAAAGTTCAATTGGAAACAGAAAGAA 120
Db |||
Qy 121 TGGATTTATCTGCTCTGCGCTGAGAGTACAAATGTCATTAATGCTATGCGAGAA 180
Db |||
Qy 121 TGGATTTATCTGCTCTGCGCTGAGAGTACAAATGTCATTAATGCTATGCGAGAA 180
Db |||
Qy 181 TCTTAGAGTGTCCATCTCTGCTGAGTTGATCAAGGAACCTGTCTCCACAAAGTGTGACC 240
Db |||
Qy 181 TCTTAGAGTGTCCATCTCTGCTGAGTTGATCAAGGAACCTGTCTCCACAAAGTGTGACC 240
Db |||
Qy 241 ACATATTTGCAATTTGCTGCTGAGTGTGAACTTCTCAACCGAGAAAGGCGCTTCACAGT 300
Db |||
Qy 241 ACATATTTGCAATTTGCTGCTGAGTGTGAACTTCTCAACCGAGAAAGGCGCTTCACAGT 300
Db |||
Qy 301 GTCTTTATGTAAGATGATATAACCAAGAGGCTTACAGAAAGTACGAGATTTAGTC 360
Db |||
Qy 301 GTCTTTATGTAAGATGATATAACCAAGAGGCTTACAGAAAGTACGAGATTTAGTC 360
Db |||
Qy 361 AACTGTTGAGAGCTATGAAATTCATTTGCTGCTTTTACGCTTGAACAGGTTTGAGT 420
Db |||
Qy 361 AACTGTTGAGAGCTATGAAATTCATTTGCTGCTTTTACGCTTGAACAGGTTTGAGT 420
Db |||
Qy 421 ATGCAACAGCTATATTTTCCAAAAGAGGAAATACTCTCTGCAATCTAAAGATG 480
Db |||
Qy 421 ATGCAACAGCTATATTTTCCAAAAGAGGAAATACTCTCTGCAATCTAAAGATG 480
Db |||
Qy 481 AAGTTTCTATCATCCAAAGTATGGCTACAGAAACCGTGCCAAAAGACTTCTACAGAGT 540
Db |||
Qy 481 AAGTTTCTATCATCCAAAGTATGGCTACAGAAACCGTGCCAAAAGACTTCTACAGAGT 540
Db |||
Qy 541 AACCAGAAATCCTTCTGAGAGAAACAGTCTCAGTGTCCACTCTCAACCTTGAA 600
Db |||
Qy 541 AACCAGAAATCCTTCTGAGAGAAACAGTCTCAGTGTCCACTCTCAACCTTGAA 600
Db |||
Qy 601 CTGTGAGAACTCTGAGGACAAAGCAGCGGATACAACTCTCAAGAGAGCTCTGTCTACATTG 660
Db |||
Qy 601 CTGTGAGAACTCTGAGGACAAAGCAGCGGATACAACTCTCAAGAGAGCTCTGTCTACATTG 660
Db |||
Qy 661 AATTGGGATCTGATTTCTGAGATACCGTTATAGGCACTTATGCGAGTGGGAG 720
Db |||
Qy 661 AATTGGGATCTGATTTCTGAGATACCGTTATAGGCACTTATGCGAGTGGGAG 720
Db |||
Qy 721 ATCAAGAAATTTGTAACAAATCAACCTCAAGGAAACAGGATGAAATCAGTTTGGATTCTG 780
Db |||
Qy 721 ATCAAGAAATTTGTAACAAATCAACCTCAAGGAAACAGGATGAAATCAGTTTGGATTCTG 780
Db |||
Qy 781 CAAAAGAGCTCTGTGAAATTTCTGAGCGGATGTAACAAATCTGACATCATCAAC 840
Db |||
Qy 781 CAAAAGAGCTCTGTGAAATTTCTGAGCGGATGTAACAAATCTGACATCATCAAC 840
Db |||
Qy 841 CCAGTAAATGATTTGAACCACTGAGAGAGCTGAGAGGATCTCTCTACAGGATTC 900
Db |||
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Db 841 CCAGTAAATGATTTGAACACACCTGAGAGGCTGCTGAGAGGCTATCCAGAAAGT 900
Qy 901 ATCAGGAGTGTCTGTTTCAAACTTGCATGTGAGGCACTGTGCAAAATCTCATGCCA 960
Db |||
Qy 901 ATCAGGAGTGTCTGTTTCAAACTTGCATGTGAGGCACTGTGCAAAATCTCATGCCA 960
Db |||
Qy 961 GCTCATTAACAGCATGAGAAACAGCAGTGTATTAATCTCATAAAGACAGAAATGAATGAGAA 1020
Db |||
Qy 961 GCTCATTAACAGCATGAGAAACAGCAGTGTATTAATCTCATAAAGACAGAAATGAATGAGAA 1020
Db |||
Qy 1021 AGGCTGAATTCGTATTAATAAAGCAACAGCTGGCTTAGCAAGGACCAACATACAGAT 1080
Db |||
Qy 1021 AGGCTGAATTCGTATTAATAAAGCAACAGCTGGCTTAGCAAGGACCAACATACAGAT 1080
Db |||
Qy 1081 GGGCTGGAAGTAAAGAAACATGTATGATAGAGGACTCCAGACAGAAAAAAGGAGTAG 1140
Db |||
Qy 1081 GGGCTGGAAGTAAAGAAACATGTATGATAGAGGACTCCAGACAGAAAAAAGGAGTAG 1140
Db |||
Qy 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAGATGGAATAGCAAGAACTGCGCATGCT 1200
Db |||
Qy 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAGATGGAATAGCAAGAACTGCGCATGCT 1200
Db |||
Qy 1201 CAGAGAAATCCTAGAGATCTGGAAGATGTTCTTGGATAACACTTAAATAGCAGCATTCAGA 1260
Db |||
Qy 1201 CAGAGAAATCCTAGAGATCTGGAAGATGTTCTTGGATAACACTTAAATAGCAGCATTCAGA 1260
Db |||
Qy 1261 AAGTTAATGAGTGTGTTTCCAGAGTGAATGTAAGTGTAGTCTGATGACTCACTGATG 1320
Db |||
Qy 1261 AAGTTAATGAGTGTGTTTCCAGAGTGAATGTAAGTGTAGTCTGATGACTCACTGATG 1320
Db |||
Qy 1321 GGGAGTCTCAATCAAAATGCAAGTGTGATGTTGGACGTTCTTAAATAGGAGTATG 1380
Db |||
Qy 1321 GGGAGTCTCAATCAAAATGCAAGTGTGATGTTGGACGTTCTTAAATAGGAGTATG 1380
Db |||
Qy 1381 AATATTCTGTTCTTCAGAGAAATAAGACTTACTGCGCAGTGTATCTCAAGGCTTTAA 1440
Db |||
Qy 1381 AATATTCTGTTCTTCAGAGAAATAAGACTTACTGCGCAGTGTATCTCAAGGCTTTAA 1440
Db |||
Qy 1441 TATGTAAGTGTGAAGAGTCTCACTCCAAATCAGTAGAGTATATTTAGAGCAAAATAT 1500
Db |||
Qy 1441 TATGTAAGTGTGAAGAGTCTCACTCCAAATCAGTAGAGTATATTTAGAGCAAAATAT 1500
Db |||
Qy 1501 TTGGGAAACCTTATCGGAAAGAGGCAAGCTCTCCCAACTTAAAGCCATGTAACCTGAAATC 1560
Db |||
Qy 1501 TTGGGAAACCTTATCGGAAAGAGGCAAGCTCTCCCAACTTAAAGCCATGTAACCTGAAATC 1560
Db |||
Qy 1561 TAAATTATGAGGATTTGTTACTGAGCCACAGATATACAGAGCGTCCCTCACAATA 1620
Db |||
Qy 1561 TAAATTATGAGGATTTGTTACTGAGCCACAGATATACAGAGCGTCCCTCACAATA 1620
Db |||
Qy 1621 AATTAAAGCTTAAAGGAGACCTTACATCAGGCTTCTCATCTGAGGATTTTATCAAGAAAG 1680
Db |||
Qy 1621 AATTAAAGCTTAAAGGAGACCTTACATCAGGCTTCTCATCTGAGGATTTTATCAAGAAAG 1680
Db |||
Qy 1681 CAGATTGCGAGTTCAAAAGACTCTCTGAAATGATTAATCGGAACTTAACCAACGAGC 1740
Db |||
Qy 1681 CAGATTGCGAGTTCAAAAGACTCTCTGAAATGATTAATCGGAACTTAACCAACGAGC 1740
Db |||
Qy 1741 AGAATGCTCAAGTGTATGATTTACTTAATAGTGTCTATGAGATATAAACAAGAGTGTATT 1800
Db |||
Qy 1741 AGAATGCTCAAGTGTATGATTTACTTAATAGTGTCTATGAGATATAAACAAGAGTGTATT 1800
Db |||
Qy 1801 CTAATTGAGAAAGAAAAATCTTAACCCCAATAGAATCACTCGAAAAAGAAATCTGCTTTCA 1860
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Db |||
Qy 1861 AAACGAAAGCTGAACCTTATAAGCAGCAGTATAGCAATATGGAATCGGAATTAATATCC 1920
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Db |||
Qy 1921 ACAATTTCAAAAGCACTTAAAAAGAAATAGGCTGAGGAGGAGTCTTCTACAGGCAATATTC 1980
Db |||
Qy 1921 ACAATTTCAAAAGCACTTAAAAAGAAATAGGCTGAGGAGGAGTCTTCTACAGGCAATATTC 1980
Db |||
```







XX AAC60793 to AAC60795 encode the human BRCA1 (omil-3) proteins given in  
CC AAB24217 to AAB24219 respectively. BRCA1 is found on chromosome 17  
CC mapping to position 17q21. The BRCA1 (omil2) coding sequence is  
CC specifically claimed in the present invention. The BRCA1 (omil2) coding  
CC sequence is useful in gene therapy, especially for preventing or treating  
CC breast or ovarian cancer. It is also useful for diagnosing or monitoring  
CC breast or ovarian cancer. Furthermore, the BRCA1 (omil2) coding sequence  
CC is useful for: (a) identifying individuals having BRCA1 gene mutations  
CC and having an increased genetic susceptibility to breast or ovarian  
CC cancer, or identifying a mutation that increases the genetic  
CC susceptibility to breast or ovarian cancer; (b) avoiding  
CC misinterpretation of polymorphisms found in the BRCA1 gene; (c)  
CC determining the presence of a previously unknown mutation in the BRCA1  
CC gene; (d) probing a human sample of the BRCA1 gene by allele to determine  
CC the presence of either polymorphic alleles or mutations; and (e)  
CC performing diagnosis with a reagent derived from the BRCA1 (omil) cDNA  
CC sequence. AAC60796 to AAC60861 represent PCR primers for the BRCA1 gene,  
CC which are used in an example from the present invention  
XX  
SQ Sequence 5711 BP; 1953 A; 1098 C; 1277 G; 1383 T; 0 U; 0 Other;  
  
Query Match 100.0%; Score 5711; DB 3; Length 5711;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 5711; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 AGCTGCTGAGACTTCTGTGACCCGCCACAGGCTGTGGGTTCTCAGATACCTGGCC 60  
DB |||||  
QY 61 CTTGGCTCAGAGGCTTCACTCTGCTCTGGTAAAGTTCAATGGAAACAGAAAGAA 120  
DB |||||  
QY 121 TGCATTTATCTGCTCTGCTGAGAGTCAAGAGTCAAAATGTCATATGTCACAGAAA 180  
DB |||||  
QY 181 TCTTAGAGTCTCCATCTGCTGAGTTGATCAAGAACTCTGCTCACAAGAGTGTGACC 240  
DB |||||  
QY 241 ACATATTTGCAATTTTGATGCTGCTGAACTTCTCAACGAGAGAAAGGCTTCACAGT 300  
DB |||||  
QY 301 GTCTTTATCTAGATGATATACCAAGAGAGCTCAAGAAAGTACAGATTTAGTC 360  
QY 361 AACTTGTGAGAGCTATTGAAATCAATTTGTGCTTTTCAGCTTGACACAGGTTTGGAGT 420  
DB |||||  
QY 421 ATGCAACAGCTATAATTTTGCAAAAGAGAAATTAATCTCTCTGACATCTTAAAGATG 480  
DB |||||  
QY 481 AAGTTTCTATCATCTCAAGATGATGGCTACAGAAACCGTGCCAAAGAGCTTCTACAGATG 540  
DB |||||  
QY 541 AACCGAATCTCTCTGACAGAACAGTCTCAGTGTCCAACTCTCTAACCTTGGAA 600  
DB |||||  
QY 601 CTGTGAGACTCTGAGGACAAAGCAGCGGATACAACTCAAAAGAGCTCTGTCTACATTTG 660  
DB |||||  
QY 661 AATTGGATCTGATTTCTTCTGAGATACCTTTAAGGCAACTTATTTGAGGCTGTGGAG 720  
DB |||||  
QY 661 AATTGGATCTGATTTCTTCTGAGATACCTTTAAGGCAACTTATTTGAGGCTGTGGAG 720  
DB |||||

QY 721 ATCAAGAAATTTGTACAAATCACTCCCTCAAGGAACCCAGGATGAAATCACTTTGGATCTTG 780  
DB |||||  
QY 781 CAAAGAGGCTCTGTGAAATTTCTGAGACCGGATGTAACAAATCTGACATCATCAAC 840  
DB |||||  
QY 841 CCAAGTAATTAATGTTGAACACCACTGAGAAGCGTGCAGCTGAGAGGCAATCCAGAAAAGT 900  
DB |||||  
QY 901 ATCAGGTAATTTCTGTTTCAAACTGTCATGTCGAGCCATGTGGCACAATATCTCATGCCA 960  
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QY 961 GCTCATTACAGCATCAGAAACAGCAGTTTATTAATCACTAAACACAGAAATGAATGTAGAAA 1020  
DB |||||  
QY 1021 AGGCTGAATTTCTGTAATAAAAGCAACAGCTTGGCTTAGCAAGGAGCCCAACATAACAGAT 1080  
DB |||||  
QY 1081 GGGCTGGAAGTAAGGAAACATGTAATGATAGCGGACTCCACAGCACAGAAAAAGGCTAG 1140  
DB |||||  
QY 1141 ATCTGAATGCTGATCCCTCTGTCGAGAGAAAGAAATGGAATGAAGCAGAAAACTGCCATGT 1200  
DB |||||  
QY 1201 CAGAGAACTCTAGACTGAGAGTCTGCTTCTGTAACACTTAATAGCAGCANTTCAGA 1260  
DB |||||  
QY 1261 AAGTTAAATGAGTGGTTTCCAGAGTGTGAATGTTAGTTCTCATGACTCAGCATGATG 1320  
DB |||||  
QY 1321 GGGAGTCTGAATCAAAATGCCAAAGTAGCTGATGTAATGGAAGTCTTAATAGAGTAGATG 1380  
DB |||||  
QY 1381 AATATTTCTGTTCTTCAGAGAAAAATAGACTTCTGCGCCAGTGTCTCATGAGGCTTTAA 1440  
DB |||||  
QY 1441 TATGTAAGAGTGAAGAGTTCACTCCAAATCAGTAGAGAGTAAATTTGAAGACAAATAT 1500  
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QY 1501 TTGGGAACCTTATCGAGAGAGGCAAGCTCCCACTTAAGCCATGTAACCTGAAATC 1560  
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QY 1561 TAATATAGGAGCATTTGTTACTGAGCCACAGATTAATCAAGAGGCTGCCCTCACAATA 1620  
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QY 1621 AATTAAGGTAAGAGAGAGCTTATCATCAGGCTTCTCATCAGGCTTTTATCAGAGAG 1680  
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QY 1681 CAGATTTGSCAGTTCAAAAGACTCTCTGAAATGATAAATCAGGGAATTAACCAAAAGGAGC 1740  
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QY 1741 AGAATGGTCAAGTGTATGATTAATTAATAGTGTCTGATGAGATTAACCAAAAGGCTGAT 1800  
DB |||||  
QY 1800 AGAATGGTCAAGTGTATGATTAATTAATAGTGTCTGATGAGATTAACCAAAAGGCTGAT 1800  
DB |||||



Db	3961	AGGAACATCACCTTAGTGGAGAAACAAATGTTCTGTAGCTTGTTCCTTCAAGTGA	4020
Qy	4021	GTGAATGGAAGACTTGACTGCAAAATACAAACACCCAGATCCTTCTTGTGATGTTCTT	4080
Db	4021	GTGAATGGAAGACTTGACTGCAAAATACAAACACCCAGATCCTTCTTGTGATGTTCTT	4080
Qy	4081	CCAAACAAATGAGGATCAGTCTGAAAGCCAGGAGTTGGTCTGATGACAGGAATGG	4140
Db	4081	CCAAACAAATGAGGATCAGTCTGAAAGCCAGGAGTTGGTCTGATGACAGGAATGG	4140
Qy	4141	TTTCAGATGATGAAGAGAGAACCGGCTTGGAAGAAATAATCAAGAAGGCAAGCA	4200
Db	4141	TTTCAGATGATGAAGAGAGAACCGGCTTGGAAGAAATAATCAAGAAGGCAAGCA	4200
Qy	4201	TGGATTTCAACTTAGGTGAGGACGATCTGGGTGTGAGGTGAACAGAGCTCTCTGAAG	4260
Db	4201	TGGATTTCAACTTAGGTGAGGACGATCTGGGTGTGAGGTGAACAGAGCTCTCTGAAG	4260
Qy	4261	ACTGCTCAGGGCTATCTCTCAGAGTGACATTTTAAACCACTCAGCAGAGGATACCATGC	4320
Db	4261	ACTGCTCAGGGCTATCTCTCAGAGTGACATTTTAAACCACTCAGCAGAGGATACCATGC	4320
Qy	4321	AACATACTGATTAAGCTCCAGCAGGAATGGCTGAACCTAGAGCTGTGTAGAACGC	4380
Db	4321	AACATACTGATTAAGCTCCAGCAGGAATGGCTGAACCTAGAGCTGTGTAGAACGC	4380
Qy	4381	ATGGAGCCAGCCTTCTAACAGCTACCTTCCATCATTAAGTGACTCTTCTGCCCTTGAAG	4440
Db	4381	ATGGAGCCAGCCTTCTAACAGCTACCTTCCATCATTAAGTGACTCTTCTGCCCTTGAAG	4440
Qy	4441	ACCTCGAAATCCAGAACAAAGCAGATCAGAAAAGAGTATTAATCTTACAGAAAAGTA	4500
Db	4441	ACCTCGAAATCCAGAACAAAGCAGATCAGAAAAGAGTATTAATCTTACAGAAAAGTA	4500
Qy	4501	GTGAATACCTTATTAAGCCAGAAATCCAGAGGCTTTCTGTGACAGAGTTTTCAGGTGCTG	4560
Db	4501	GTGAATACCTTATTAAGCCAGAAATCCAGAGGCTTTCTGTGACAGAGTTTTCAGGTGCTG	4560
Qy	4561	CAGATAGTTCTACAGTAAAAATAAAGAACAGAGTGAAAGTCAATCCCTTCTAAAT	4620
Db	4561	CAGATAGTTCTACAGTAAAAATAAAGAACAGAGTGAAAGTCAATCCCTTCTAAAT	4620
Qy	4621	GCCATCATTAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	4680
Db	4621	GCCATCATTAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	4680
Qy	4681	ACTACCCATCTCAAGAGGAGTCAATTAAGTGTGATGATGATGATGATGATGATGATG	4740
Db	4681	ACTACCCATCTCAAGAGGAGTCAATTAAGTGTGATGATGATGATGATGATGATGATG	4740
Qy	4741	AGTCTGGGCCACAGATTTGAGGAAACATCTTACTTGTGATGATGATGATGATGATGATG	4800
Db	4741	AGTCTGGGCCACAGATTTGAGGAAACATCTTACTTGTGATGATGATGATGATGATGATG	4800
Qy	4801	CCCCTTACCTGGAATCTGGAATCAGCCTCTTCTGATGATGATGATGATGATGATGATG	4860
Db	4801	CCCCTTACCTGGAATCTGGAATCAGCCTCTTCTGATGATGATGATGATGATGATGATG	4860
Qy	4861	AAGCAGAGCCCAAGATCAGTGTGTGTCGAAATACATACATCTTCAACCTCTGCAATGA	4920
Db	4861	AAGCAGAGCCCAAGATCAGTGTGTGTCGAAATACATACATCTTCAACCTCTGCAATGA	4920
Qy	4921	AAGTTCCTCCCAATTCAGAAATGTCAGATCTGCCCCAGGCTCCAGCTGCTGCTCACTACTG	4980
Db	4921	AAGTTCCTCCCAATTCAGAAATGTCAGATCTGCCCCAGGCTCCAGCTGCTGCTCACTACTG	4980
Qy	4981	ATACCTCTGGGTATTAATGCAATGGAAGAAAGTGTGACAGGAGAAACCCAGAAATGACAG	5040
Db	4981	ATACCTCTGGGTATTAATGCAATGGAAGAAAGTGTGACAGGAGAAACCCAGAAATGACAG	5040
Qy	5041	CTTCAACAGAAAGGCTCAACAAAGATGTCAGGTGTGCTGCTGCTGCTGCTGCTGCTGCTG	5100
Db	5041	CTTCAACAGAAAGGCTCAACAAAGATGTCAGGTGTGCTGCTGCTGCTGCTGCTGCTGCTG	5100
Qy	5101	AAATTAATGCTGCTGTAACAAGTTTCCAGAGAAACCAATCATCATCTTTAACTTAATCTAATTA	5160
Db	5101	AAATTAATGCTGCTGTAACAAGTTTCCAGAGAAACCAATCATCATCTTTAACTTAATCTAATTA	5160
Qy	5161	CTGAAGAGACTTACTCATGTTTATGAAACAGATGCTGAGTTTGTGTGAAACGGACAC	5220
Db	5161	CTGAAGAGACTTACTCATGTTTATGAAACAGATGCTGAGTTTGTGTGAAACGGACAC	5220
Qy	5221	TGAATAATTTTCTAGGAATTCGGGAGGAAATGGGTAGTTAGTATTTCTTGGGTGACCC	5280
Db	5221	TGAATAATTTTCTAGGAATTCGGGAGGAAATGGGTAGTTAGTATTTCTTGGGTGACCC	5280
Qy	5281	AGTCTATTAAAGAAAGAAATCTGAATGAGCATGATTTTGAAGTCAGAGGAGATGAG	5340
Db	5281	AGTCTATTAAAGAAAGAAATCTGAATGAGCATGATTTTGAAGTCAGAGGAGATGAG	5340
Qy	5341	TCATGGAAGAAACCAACCAAGGTCCTCAAGGAGCAGAGAAATCCAGGACAGAAAGATCT	5400
Db	5341	TCATGGAAGAAACCAACCAAGGTCCTCAAGGAGCAGAGAAATCCAGGACAGAAAGATCT	5400
Qy	5401	TCAGGGGGCTAGAAATCTGTGCTATGGGCTTTCACCAACATGCCCAAGATCAACTGG	5460
Db	5401	TCAGGGGGCTAGAAATCTGTGCTATGGGCTTTCACCAACATGCCCAAGATCAACTGG	5460
Qy	5461	AAATGATGTACAGCTGTGTGCTTCTGTGTGTAAGGAGCTTTTCATCTTCACTTCACTTGG	5520
Db	5461	AAATGATGTACAGCTGTGTGCTTCTGTGTGTAAGGAGCTTTTCATCTTCACTTCACTTGG	5520
Qy	5521	GCACAGGTGTCACCCAAATTTGTGTTGTGAGCCAGATGCTGCAAGAGCAATGGCT	5580
Db	5521	GCACAGGTGTCACCCAAATTTGTGTTGTGAGCCAGATGCTGCAAGAGCAATGGCT	5580
Qy	5581	TCCATGCAATTTGGCAGATGTGTGAGGACCTGTGTGACCCAGAGAGTGGTGTGGACA	5640
Db	5581	TCCATGCAATTTGGCAGATGTGTGAGGACCTGTGTGACCCAGAGAGTGGTGTGGACA	5640
Qy	5641	GTGTAGCACTCTACAGTGCACAGAGCTGACACCTTACCTGATACCCAGATCCCCACA	5700
Db	5641	GTGTAGCACTCTACAGTGCACAGAGCTGACACCTTACCTGATACCCAGATCCCCACA	5700
Qy	5701	GCCACTACTGA 5711	
Db	5701	GCCACTACTGA 5711	
RESULT 3			
ACA61333			
ID	ACA61333 standard; cDNA; 5711 BP.		
XX	ACA61333;		
AC	ACA61333;		
DT	07-AUG-2003 (first entry)		
XX	Human BRCA1 allele omi2, cDNA.		
DE	Human; ss; gene; BRCA1; omi2; gene therapy; tumour; breast cancer;		
KW	ovarian cancer; prostate cancer; colon cancer; SNP;		
KW	single nucleotide polymorphism.		
XX	Homo sapiens.		
OS	Homo sapiens.		
PH	Location/Qualifiers		
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FT	/product= "BRCA1 omi2"		
FT	replace(2201,C)		
FT	/*tag= b		
FT	/notes= "single nucleotide polymorphism"		
FT	replace(2430,T)		
FT	/*tag= c		
FT	/notes= "single nucleotide polymorphism"		
FT	replace(2731,C)		



1081	GGGCTGGGAAGTAAAGAAACATCTAATGATAGCGGCACTCCGACGACAGAAAAAGGTAG	1140
1141	ATCTGAATGCTGATCCCTCTGTGTGAGAGAAAAAGAAATGGAATAAGCAGAAAACTGCCATGCT	1200
1141	ATCTGAATGCTGATCCCTCTGTGTGAGAGAAAAAGAAATGGAATAAGCAGAAAACTGCCATGCT	1200
1201	CAGAGAACTCTAGAGATCTGAGAGATGTTCTCTTGATTAACACTAAATAGCAGCAATTCAGA	1260
1201	CAGAGAACTCTAGAGATCTGAGAGATGTTCTCTTGATTAACACTAAATAGCAGCAATTCAGA	1260
1261	AAGTTAATAGTGGTGTTCCTCAGAACTGATGAACCTTTAGGTTCTGATGACTCACATGATG	1320
1261	AAGTTAATAGTGGTGTTCCTCAGAACTGATGAACCTTTAGGTTCTGATGACTCACATGATG	1320
1321	GGGAGTCTGAATCAAAATGCCAAAAGTAGCTGATGTATTTGCGAGTTCTTAAATGAGGTAGATG	1380
1321	GGGAGTCTGAATCAAAATGCCAAAAGTAGCTGATGTATTTGCGAGTTCTTAAATGAGGTAGATG	1380
1381	AATATTCTGGTCTTTTCAGAGAAAAATAGACTTACTTGGCCAGTGAATCCTCATGAGGCTTAA	1440
1381	AATATTCTGGTCTTTTCAGAGAAAAATAGACTTACTTGGCCAGTGAATCCTCATGAGGCTTAA	1440
1441	TATGTAAAGGTAAAGAGTTCACTCCAAATCAGTAGAGAGTAATATTTGAAGACAAAATAT	1500
1441	TATGTAAAGGTAAAGAGTTCACTCCAAATCAGTAGAGAGTAATATTTGAAGACAAAATAT	1500
1501	TTGGGAAACCTTATCGGAGAGGAGCAAGCCCTCCCACTTAAGCCATGTACTGCAATTC	1560
1501	TTGGGAAACCTTATCGGAGAGGAGCAAGCCCTCCCACTTAAGCCATGTACTGCAATTC	1560
1561	TAATTTATAGGAGCAATTTCTTACTGAGCCACAGATAATAAAGAGCGTCCCTCCACAAATA	1620
1561	TAATTTATAGGAGCAATTTCTTACTGAGCCACAGATAATAAAGAGCGTCCCTCCACAAATA	1620
1621	AATTAAGGCTTAAGAGGAGACTTACATCAGCGCTTCATCTCTGAGATTTTATTAAGAAAG	1680
1621	AATTAAGGCTTAAGAGGAGACTTACATCAGCGCTTCATCTCTGAGATTTTATTAAGAAAG	1680
1681	CAGATTTGGCAGTTTCAAAAGACTCTCTGAAATGATAAATCAGGAACTTAAACCAACGAGC	1740
1681	CAGATTTGGCAGTTTCAAAAGACTCTCTGAAATGATAAATCAGGAACTTAAACCAACGAGC	1740
1741	AGATTTGCTCAAGTGAATGAATTAATTAATGTTGTCATGAGATAAATAACAAAAGTGAT	1800
1741	AGATTTGCTCAAGTGAATGAATTAATTAATGTTGTCATGAGATAAATAACAAAAGTGAT	1800
1801	CTATTTCAGAAATGAGAAAAATCCTTAACCCAAATAGAAATCACTTCGAAAAAGAAATTCGCTTCA	1860
1801	CTATTTCAGAAATGAGAAAAATCCTTAACCCAAATAGAAATCACTTCGAAAAAGAAATTCGCTTCA	1860
1861	AAAACGAAAGCTGAACTTATAGCAGCAGTATTAAGCAATATGGAATCTCGAAATTAATAATCC	1920
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1921	ACAATTCAAAGCACCCTTAAAGAAATAGGCTTGAGGAGAGTCTTCTTACAGGCAATATTC	1980
1921	ACAATTCAAAGCACCCTTAAAGAAATAGGCTTGAGGAGAGTCTTCTTACAGGCAATATTC	1980
1981	ATGCGCTTGAACCTAGTAGTCACTAGAAATCTTAAGCCCACTTAATTTGACTGAAATTCGAAA	2040
1981	ATGCGCTTGAACCTAGTAGTCACTAGAAATCTTAAGCCCACTTAATTTGACTGAAATTCGAAA	2040
2041	TTGATAGTTGTTCTAGCAGTGAAGAGATAAAGAAAAAAAGTACAACCAATGCCAGTCA	2100
2041	TTGATAGTTGTTCTAGCAGTGAAGAGATAAAGAAAAAAAGTACAACCAATGCCAGTCA	2100
2101	GGCACACAGAAACCTTACACTCATGGAAGGTAAAGAACTCGAACTGGAGGCCAAGAGA	2160
2101	GGCACACAGAAACCTTACACTCATGGAAGGTAAAGAACTCGAACTGGAGGCCAAGAGA	2160
2161	GTAAACAAGCCAAATGAACAGACAAGTAAAGACATGACAGTGATCTTTTCCCAGAGCTGA	2220
2161	GTAAACAAGCCAAATGAACAGACAAGTAAAGACATGACAGTGATCTTTTCCCAGAGCTGA	2220

QY	2221	AGTTAAACAAATGCACCTGGTCTCTTTTACTAAGTGTTCAAATACACAGTGAACCTTAAAGAAAT	2280
DB	2221	AGTTAAACAAATGCACCTGGTCTCTTTTACTAAGTGTTCAAATACACAGTGAACCTTAAAGAAAT	2280
QY	2281	TTGTCAATCTCTAGCTTCCAAAGAGAAAGAAAAGAGAGAACTAGAAAACAGTTTAAAGTGT	2340
DB	2281	TTGTCAATCTCTAGCTTCCAAAGAGAGAAAGAAAAGAGAGAACTAGAAAACAGTTTAAAGTGT	2340
QY	2341	CTAATAAGTCTGAGAGACCCCAAGATCTCATGTTTAAGTGGAGAAAGGGTTTTGCAAACTG	2400
DB	2341	CTAATAAGTCTGAGAGACCCCAAGATCTCATGTTTAAGTGGAGAAAGGGTTTTGCAAACTG	2400
QY	2401	AAAGATCTGTAGAGAGTAGCAGTATTTTCACTGGTACCTGGTACTGTATTAATGGCACTCAGG	2460
DB	2401	AAAGATCTGTAGAGAGTAGCAGTATTTTCACTGGTACCTGGTACTGTATTAATGGCACTCAGG	2460
QY	2461	AAAGTATCTCTTACTTGGAGTTAGCACTCTTAGGGAGGCCAAAGACAGACCAATAAAT	2520
DB	2461	AAAGTATCTCTTACTTGGAGTTAGCACTCTTAGGGAGGCCAAAGACAGACCAATAAAT	2520
QY	2521	GTGTGAGTCAGTGTGCAGCATTTTGAAAACCCCAAGGGACTAAATTCATGGTGTGTCCAAAG	2580
DB	2521	GTGTGAGTCAGTGTGCAGCATTTTGAAAACCCCAAGGGACTAAATTCATGGTGTGTCCAAAG	2580
QY	2581	ATATAGAGAAATGACACAGAGAGGCTTTAAGTATCCATTTGGGACATGAGTTTAAACAGATC	2640
DB	2581	ATATAGAGAAATGACACAGAGAGGCTTTAAGTATCCATTTGGGACATGAGTTTAAACAGATC	2640
QY	2641	GGGAAACAAGCATAGAAATGGAGAAAGTGAACCTTGATGCTCAGTATTTGCAGAAATACAT	2700
DB	2641	GGGAAACAAGCATAGAAATGGAGAAAGTGAACCTTGATGCTCAGTATTTGCAGAAATACAT	2700
QY	2701	TCAAGGTTTCAAAGGCCAGTCATTTCTGCTCTGTTTTTCAAATCCAGGAAATGCAGAGAGAGG	2760
DB	2701	TCAAGGTTTCAAAGGCCAGTCATTTCTGCTCTGTTTTTCAAATCCAGGAAATGCAGAGAGAGG	2760
QY	2761	AATGTCACATTCCTGCCCCACTCTGGGFCCTTAAAGAGAAACAAAGTCCAAAAGTCACATT	2820
DB	2761	AATGTCACATTCCTGCCCCACTCTGGGFCCTTAAAGAGAAACAAAGTCCAAAAGTCACATT	2820
QY	2821	TTGAAATGTGAACAAAGAGAGAAATCAAGGAAAGAAATGAGTCTTAATATCAAGCCCTGTAC	2880
DB	2821	TTGAAATGTGAACAAAGAGAGAAATCAAGGAAAGAAATGAGTCTTAATATCAAGCCCTGTAC	2880
QY	2881	AGA CAGTTAATATCATGCAAGCTTTCCTGTGTTGGT CAGAAAAGATAGCCAGTTTGATA	2940
DB	2881	AGA CAGTTAATATCATGCAAGCTTTCCTGTGTTGGT CAGAAAAGATAGCCAGTTTGATA	2940
QY	2941	ATGCCAAATGTAGTATCAAAGGAGGCTCTAGGTTTTGTTCTATCATCTCAGTTTTCAGAGGCA	3000
DB	2941	ATGCCAAATGTAGTATCAAAGGAGGCTCTAGGTTTTGTTCTATCATCTCAGTTTTCAGAGGCA	3000
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DB	3001	ACGAAACTGGACTCATTTACTCCTCAAATTAACATGGACTTTTACAAAACCCATATCGGTATAC	3060
QY	3061	CACCACCTTTTCCCATCAAGTCAATTTGTTTAAACTAAATGTTAAGAAAATCTGCTAGAGG	3120
DB	3061	CACCACCTTTTCCCATCAAGTCAATTTGTTTAAACTAAATGTTAAGAAAATCTGCTAGAGG	3120
QY	3121	AAAACTTTTAGGAAACATTTCAATGTCACTGAAAGAGAAATGGGAAATGAGAAACATTTCCAA	3180
DB	3121	AAAACTTTTAGGAAACATTTCAATGTCACTGAAAGAGAAATGGGAAATGAGAAACATTTCCAA	3180
QY	3181	GTACAGTGAGCACAATTTAGCCGTAAATAACATTAGAGAAAATGTTTTTAAAGGAGCGAGCT	3240
DB	3181	GTACAGTGAGCACAATTTAGCCGTAAATAACATTAGAGAAAATGTTTTTAAAGGAGCGAGCT	3240
QY	3241	CAAGCAATAATTAAGTAGTAGGTTCCAGTACTAATGAAGTGGGCTCCAGTATTAATGAAA	3300
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Db 3661 TCCAGAGGAGAGCTTAGCAGGAGTCTAGCCCTTTTACCCTTACCACTACACATTTGCTCAGG 3720  
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Db 4741 AGTCTGGGCCACACAGATTTGACGAAACATCTTTATCTTGCAAGGCAAGATCTAGAGGAA 4800  
Qy 4801 CCGCTTACCTGGAATCTGGAATCAGGCTCTTCTGATGACCTGATCTGATCTCTCTCTG 4860  
Db 4801 CCGCTTACCTGGAATCTGGAATCAGGCTCTTCTGATGACCTGATCTGATCTCTCTCTG 4860  
Qy 4861 AAGCAGAGCCCCAGAGTCTGCTGTTGGCAACATACCATCTTCAACCTCTGCAATTGA 4920  
Db 4861 AAGCAGAGCCCCAGAGTCTGCTGTTGGCAACATACCATCTTCAACCTCTGCAATTGA 4920  
Qy 4921 AAGTCTCCCAATTTGAAGTTGCAGATCTGCCAGGCTCCAGCTGCTGCTCATACTACTG 4980  
Db 4921 AAGTCTCCCAATTTGAAGTTGCAGATCTGCCAGGCTCCAGCTGCTGCTCATACTACTG 4980  
Qy 4981 ATACTCTGGTATATGCAATGGAAGAAAGTGTGACAGGAGGAGAGGAGGAGGAGGAGGAG 5040  
Db 4981 ATACTCTGGTATATGCAATGGAAGAAAGTGTGACAGGAGGAGAGGAGGAGGAGGAGGAG 5040  
Qy 5041 CTTCAACAGAAAGGCTCAACAAAGAAATGTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5100  
Db 5041 CTTCAACAGAAAGGCTCAACAAAGAAATGTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5100  
Qy 5101 AATTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5160  
Db 5101 AATTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5160  
Qy 5161 CTGAAGAGACTACTCATGTTTATGAAACACAGATGCTGAGTTTGTGTTGTTGTTGTTGTTG 5220  
Db 5161 CTGAAGAGACTACTCATGTTTATGAAACACAGATGCTGAGTTTGTGTTGTTGTTGTTGTTG 5220  
Qy 5221 TGAATATTTTCTAGGAATGGGGAGGAAATGGGTAGTGTAGCTATTTCTTCTGCTGCTGCTG 5280  
Db 5221 TGAATATTTTCTAGGAATGGGGAGGAAATGGGTAGTGTAGCTATTTCTTCTGCTGCTGCTG 5280  
Qy 5281 AGTCTATTAAAGAAAGAAATGCTGAAATGAGCATGATTTTGAAGTCAGAGGAGATGTGG 5340  
Db 5281 AGTCTATTAAAGAAAGAAATGCTGAAATGAGCATGATTTTGAAGTCAGAGGAGATGTGG 5340  
Qy 5341 TCAATGGAAGAAACCAAGGTCCTGAAAGGAGAGAAATCCAGGAGCAGAAAGATCT 5400  
Db 5341 TCAATGGAAGAAACCAAGGTCCTGAAAGGAGAGAAATCCAGGAGCAGAAAGATCT 5400  
Qy 5401 TCAGGGGGCTAGAAATCTGTTGCTATGGGCCCTTACCAACATGCCCACAGATCAACTGG 5460  
Db 5401 TCAGGGGGCTAGAAATCTGTTGCTATGGGCCCTTACCAACATGCCCACAGATCAACTGG 5460  
Qy 5461 AATGGAATGATCAGCTGT 5520

Db	5461	AATGATGGTACAGCTGTGTGGTGCTTCCTGTGGGTGAAGAGACTTTTCATCATTCACCCCTTG	5520
Qy	5521	GCACAGGTGTCCACCATAATTGTGGTTGTGCGAGCCAGATGCCCTGCACGAGGACAATGGCT	5580
Db	5521	GCACAGGTGTCCACCATAATTGTGGTTGTGCGAGCCAGATGCCCTGCACGAGGACAATGGCT	5580
Qy	5581	TCCATGCATAATTGGGCGAGATGTGTGAGGCACCTGTGTGGTGAACCCGAGAGTGGGTGTTGGACA	5640
Db	5581	TCCATGCATAATTGGGCGAGATGTGTGAGGCACCTGTGTGGTGAACCCGAGAGTGGGTGTTGGACA	5640
Qy	5641	GTGTAGCACTCTTACCAGTGCAGAGCTGGGACACCTACTCTGATACCCAGATCCCCCACA	5700
Db	5641	GTGTAGCACTCTTACCAGTGCAGAGCTGGGACACCTACTCTGATACCCAGATCCCCCACA	5700
Qy	5701	GCCACTACTGA	5711
Db	5701	GCCACTACTGA	5711

RESULT 4  
 ADC63291  
 ID ADC63291 standard; cDNA; 5711 BP.  
 XX AC AC  
 XX XX  
 DT 18-DEC-2003 (first entry)  
 DE Polymorphic cDNA sequence (om13) for human BRCA1.  
 XX Human; BRCA1; om13; gene pool; gene therapy; BRCA1 gene mutation;  
 KW breast cancer; ovarian cancer; cytostatic; chromosome 17q21; gene; BA.  
 XX Homo sapiens.  
 OS  
 XX US2002183268-A1.  
 PN  
 XX 05-DEC-2002.  
 PD  
 XX 13-DEC-2000; 2000US-00734672.  
 PF  
 XX 12-FEB-1996; 96US-00598591.  
 PR 07-NOV-1997; 97US-00966436.  
 XX (MURP/) MURPHY P D.  
 PA (ALLE/) ALLEN A C.  
 PA (ALVA/) ALVARES C P.  
 PA (CRIT/) CRITZ B S.  
 PA (OLSO/) OLSON S J.  
 PA (SCHE/) SCHELTER D B.  
 PA {ZENGE/} ZENG B.  
 XX  
 XX Murphy PD, Allen AC, Alvares CP, Critz BS, Olson SJ, Schelter DB;  
 Zeng B;  
 PI  
 PI  
 XX  
 DR WPI; 2003-765230/72.  
 DR P-PSDB; ADC63292.  
 XX  
 PT New isolated DNA sequence of the BRCA1 coding sequence, useful for the  
 PT diagnosis and treatment of disorders with BRCA1 gene mutation, such as  
 PT breast and ovarian cancer.  
 XX  
 PS Claim 5; SEQ ID NO 5; 59pp; English.  
 PS  
 CC The present invention relates to the isolation of a consensus DNA  
 CC sequencing of the human BRCA1 coding sequence (om1), and two polymorphic  
 CC coding sequences for human BRCA1 (om12 and om13). The gene encoding human  
 CC BRCA1 maps to chromosome 17q21. Also disclosed are the three proteins  
 CC encoded by these polynucleotide sequences, and a method of determining  
 CC the consensus sequence for BRCA1. Omil represents the most commonly  
 CC occurring coding sequence in the human gene pool. The coding sequences  
 CC are useful for gene therapy and can be administered by direct injection  
 CC into the tissue. The methods and compositions of the present invention  
 CC are useful for the diagnosis and treatment of disorders with BRCA1 gene  
 CC mutation.



Db	3121	AAAACTTTGAGAACATTCATGTCACCTGAAAGAGAAATGGGAAATGAGAAATTCCTCAA	3180
Qy	3181	GTACAGTGAGCACAATTAGCGGTAAATAACATTTAGAGAAAATGTTTTTAAAGGAGCCAGCT	3240
Db	3181	GTACAGTGAGCACAATTAGCGGTAAATAACATTTAGAGAAAATGTTTTTAAAGGAGCCAGCT	3240
Qy	3241	CAAGCAATATTAATGAAGTAGGTTCCAGTACTAATGAAGTGGGCTCCAGTATTAATGAAA	3300
Db	3241	CAAGCAATATTAATGAAGTAGGTTCCAGTACTAATGAAGTGGGCTCCAGTATTAATGAAA	3300
Qy	3301	TAGGTTCCAGTGATGAAAACATTCAGCAGAACTAGGTAGAAAACAGAGGGCCAAAATTGA	3360
Db	3301	TAGGTTCCAGTGATGAAAACATTCAGCAGAACTAGGTAGAAAACAGAGGGCCAAAATTGA	3360
Qy	3361	ATGCTATGCTTAGATAGGGGTTTTGCAACTGAGGTCATTAACAAAGTCTCTCCGGAA	3420
Db	3361	ATGCTATGCTTAGATAGGGGTTTTGCAACTGAGGTCATTAACAAAGTCTCTCCGGAA	3420
Qy	3421	GTAATTTGTAAGCATCTCTGAAATAAAGCAAGAAATGAAGTAGTTTCAGATGTTA	3480
Db	3421	GTAATTTGTAAGCATCTCTGAAATAAAGCAAGAAATGAAGTAGTTTCAGATGTTA	3480
Qy	3481	ATACAGATTTCTCTCGATCTGATTTTCAGATTAATTTAGACAGCCCTATGGGAGTAGTC	3540
Db	3481	ATACAGATTTCTCTCGATCTGATTTTCAGATTAATTTAGACAGCCCTATGGGAGTAGTC	3540
Qy	3541	ATGCATCTCAGGTTTGTCTGAGACACCTGATGACCTGTGTAGATGATGATGAAATTAAGG	3600
Db	3541	ATGCATCTCAGGTTTGTCTGAGACACCTGATGACCTGTGTAGATGATGATGAAATTAAGG	3600
Qy	3601	AAGATATAGTTTGTCTGAAATGAATTAAGGAAAGTTCTGCTGTTTTTAGCAAAAGCG	3660
Db	3601	AAGATATAGTTTGTCTGAAATGAATTAAGGAAAGTTCTGCTGTTTTTAGCAAAAGCG	3660
Qy	3661	TCCAGAGAGAGAGCTTAGCAGAGTCTTAGCCCTTTTACCCATACACATTTGGCTCAGG	3720
Db	3661	TCCAGAGAGAGAGCTTAGCAGAGTCTTAGCCCTTTTACCCATACACATTTGGCTCAGG	3720
Qy	3721	GTTTACCGAAGGGGCCAAGAAATTAAGTCTCTCAGAGAGAACTTATCTAGTGAGGATG	3780
Db	3721	GTTTACCGAAGGGGCCAAGAAATTAAGTCTCTCAGAGAGAACTTATCTAGTGAGGATG	3780
Qy	3781	AAGAGCTTCCCTGCTTCCACACTTGTATTGTTGTAAGTAAACAAATATACCTTCTCAGT	3840
Db	3781	AAGAGCTTCCCTGCTTCCACACTTGTATTGTTGTAAGTAAACAAATATACCTTCTCAGT	3840
Qy	3841	CTACTAGGCATAGCACCGTTGCTACCGAGTGTCTGTCTTAAGAACACAGAGAGGAAATTTAT	3900
Db	3841	CTACTAGGCATAGCACCGTTGCTACCGAGTGTCTGTCTTAAGAACACAGAGAGGAAATTTAT	3900
Qy	3901	TATCATTTGAAGATAGCTTAAATGACTGCAAGTAAACAGGTAAATTTGGCAAGGCAATCTC	3960
Db	3901	TATCATTTGAAGATAGCTTAAATGACTGCAAGTAAACAGGTAAATTTGGCAAGGCAATCTC	3960
Qy	3961	AGGAAATCACCCTTAGTGAGGAAACAAAATGTTCTGCTAGCTGTTTTTCTTCAAGTGCA	4020
Db	3961	AGGAAATCACCCTTAGTGAGGAAACAAAATGTTCTGCTAGCTGTTTTTCTTCAAGTGCA	4020
Qy	4021	GTGAATTTGGAAGACTTGACTGCAAAATCAAAACCCAGGATCCCTTCTTGAATGGTTCTT	4080
Db	4021	GTGAATTTGGAAGACTTGACTGCAAAATCAAAACCCAGGATCCCTTCTTGAATGGTTCTT	4080
Qy	4081	CCAAACAAATGAGCCATCAGTCTGAAGAGCCAGGAGTTGGTCTGAGTGCAAGGAATTTGG	4140
Db	4081	CCAAACAAATGAGCCATCAGTCTGAAGAGCCAGGAGTTGGTCTGAGTGCAAGGAATTTGG	4140
Qy	4141	TTTCAGATGATGAAGAAAGGAAACGGGCTTTGGAAGAAAATTAATCAAGAGAGCAAGCA	4200
Db	4141	TTTCAGATGATGAAGAAAGGAAACGGGCTTTGGAAGAAAATTAATCAAGAGAGCAAGCA	4200
Qy	4201	TGGATTCAACTTAGGTGAGCAGCATCTGGTGTGAGAGTGAAACAGGCTCTCTGAAG	4260
Db	4201	TGGATTCAACTTAGGTGAGCAGCATCTGGTGTGAGAGTGAAACAGGCTCTCTGAAG	4260

Qy	4261	ACTGCTCAGGGCTATCTCTCTCAGAGTGACATTTTAAACCACTCAGCAGAGGGATACCATGC	4320
Db	4261	ACTGCTCAGGGCTATCTCTCTCAGAGTGACATTTTAAACCACTCAGCAGAGGGATACCATGC	4320
Qy	4321	AACATAAACCCTATAAGCTCCAGCAGGAAATGGCTGAACCTAGAACTGTGTGTAGAACAGC	4380
Db	4321	AACATAAACCCTATAAGCTCCAGCAGGAAATGGCTGAACCTAGAACTGTGTGTAGAACAGC	4380
Qy	4381	ATGGGAGCCAGGCTTCTAAACAGTACCCCTTCCATCATTAAGTACACTTCTTGGCCCTTGAGG	4440
Db	4381	ATGGGAGCCAGGCTTCTAAACAGTACCCCTTCCATCATTAAGTACACTTCTTGGCCCTTGAGG	4440
Qy	4441	ACCTCGGAAATCCAGAAACAAAGCACATCAGAAAAGACAGTATTAACTTCACAGAAAAGTA	4500
Db	4441	ACCTCGGAAATCCAGAAACAAAGCACATCAGAAAAGACAGTATTAACTTCACAGAAAAGTA	4500
Qy	4501	GTGAATPACCTATAAGCCAGAAATCCAGAAAGGCTTCTGCTGACAAAGTTGAGGTCTCTG	4560
Db	4501	GTGAATPACCTATAAGCCAGAAATCCAGAAAGGCTTCTGCTGACAAAGTTGAGGTCTCTG	4560
Qy	4561	CAGATAGTTCTACCAAGTAAATAAAGAACACAGGAGTGAAAGTCCATCCCTTCTTAAT	4620
Db	4561	CAGATAGTTCTACCAAGTAAATAAAGAACACAGGAGTGAAAGTCCATCCCTTCTTAAT	4620
Qy	4621	GCCCATCATTAGATGATAGGTGGTACATGCACAGTTGCTCTGGGAGTCTTTCAGAAATAGAA	4680
Db	4621	GCCCATCATTAGATGATAGGTGGTACATGCACAGTTGCTCTGGGAGTCTTTCAGAAATAGAA	4680
Qy	4681	ACTACCCATCTCAAGAGGAGCTCTTAAGGTTGTTGATGTGAGGAGCAACAGCTGGAG	4740
Db	4681	ACTACCCATCTCAAGAGGAGCTCTTAAGGTTGTTGATGTGAGGAGCAACAGCTGGAG	4740
Qy	4741	AGTCTGGGCGCACACCAATTTGAAGGAAACATCTTACTTGCACAGGCAAGATCTAGAGGGAA	4800
Db	4741	AGTCTGGGCGCACACCAATTTGAAGGAAACATCTTACTTGCACAGGCAAGATCTAGAGGGAA	4800
Qy	4801	CCCCTTACCTGGAAATCTGGAAATCAGCTCTTCTCTGATGACCCCTGATCTGATCTCTG	4860
Db	4801	CCCCTTACCTGGAAATCTGGAAATCAGCTCTTCTCTGATGACCCCTGATCTGATCTCTG	4860
Qy	4861	AAGACAGAGCCCCAGAGTCAAGCTCGTGTGGCAACATACCATCTTCAACCTCTGCAATTGA	4920
Db	4861	AAGACAGAGCCCCAGAGTCAAGCTCGTGTGGCAACATACCATCTTCAACCTCTGCAATTGA	4920
Qy	4921	AAGTCCCCTCAATTTGAAGTTGAGAAATCTGCCAGGGTCCAGCTGCTGCTCATCTACTG	4980
Db	4921	AAGTCCCCTCAATTTGAAGTTGAGAAATCTGCCAGGGTCCAGCTGCTGCTCATCTACTG	4980
Qy	4981	ATACTCTGGGTATTAATGCAATGGAAAGTGTGAGCAGGGAGAGCCAGAAATTCACAG	5040
Db	4981	ATACTCTGGGTATTAATGCAATGGAAAGTGTGAGCAGGGAGAGCCAGAAATTCACAG	5040
Qy	5041	CTTCAACAGAAAAGGTTCAACAAAAGAAATGTCATGTTGGTGTCTGGCCCTGACCCAGAA	5100
Db	5041	CTTCAACAGAAAAGGTTCAACAAAAGAAATGTCATGTTGGTGTCTGGCCCTGACCCAGAA	5100
Qy	5101	AATTTATGCTGCTGTAAGTTTCCAGAAAACACACATCTACTTTAACTTAATCTAATTA	5160
Db	5101	AATTTATGCTGCTGTAAGTTTCCAGAAAACACACATCTACTTTAACTTAATCTAATTA	5160
Qy	5161	CTGAAGAGACTACTCTCATGTTGTTATGAAAACAGATCTCAGTTTGTGTGAAACGACAC	5220
Db	5161	CTGAAGAGACTACTCTCATGTTGTTATGAAAACAGATCTCAGTTTGTGTGAAACGACAC	5220
Qy	5221	TGAATATTTTCTAGGAATTTGGGGAGGAAAATGGGTAGTTAGCTATTTCTGGGTGACCCC	5280
Db	5221	TGAATATTTTCTAGGAATTTGGGGAGGAAAATGGGTAGTTAGCTATTTCTGGGTGACCCC	5280
Qy	5281	AGTCTATTTAAAGAAAGAAAATGCTGAATGAGCATGATTTTGAAGTCAAGAGAGATGCTGG	5340
Db	5281	AGTCTATTTAAAGAAAGAAAATGCTGAATGAGCATGATTTTGAAGTCAAGAGAGATGCTGG	5340

QY 5341 TCAATGGAGAAACCAACCAAGGTCCTCAAGCGAGCAAGAGATCCAGGACAGAAAGATCT 5400  
DB |||||  
QY 5341 TCAATGGAGAAACCAACCAAGGTCCTCAAGCGAGCAAGAGATCCAGGACAGAAAGATCT 5400  
DB |||||  
QY 5401 TCAGGGGGCTAGAAATCTGTTCTATGGCCCTTCAACCAACATGCCACAGATCAACTGG 5460  
DB |||||  
QY 5401 TCAGGGGGCTAGAAATCTGTTCTATGGCCCTTCAACCAACATGCCACAGATCAACTGG 5460  
DB |||||  
QY 5461 AATGGATGCTAGAGCTGTGTGTGCTTCTGTGTGAAGAGCTTTTCATCATTCACCCCTTG 5520  
DB |||||  
QY 5461 AATGGATGCTAGAGCTGTGTGTGCTTCTGTGTGAAGAGCTTTTCATCATTCACCCCTTG 5520  
DB |||||  
QY 5521 GCACAGGTGTCCACCAATTTGGTGTGTCAGCCAGATGCTTGGACAGAGCAATGGCT 5580  
DB |||||  
QY 5521 GCACAGGTGTCCACCAATTTGGTGTGTCAGCCAGATGCTTGGACAGAGCAATGGCT 5580  
DB |||||  
QY 5581 TCCATGCAATTTGGGAGATGTGTGAGGCACTGTGTGTCAGCCAGATGCTTGGACAG 5640  
DB |||||  
QY 5581 TCCATGCAATTTGGGAGATGTGTGAGGCACTGTGTGTCAGCCAGATGCTTGGACAG 5640  
DB |||||  
QY 5641 GTGTAGCACTTACCAAGTCCAGGAGCTGAGCACTTGTATGATACCCAGATGCCCCACA 5700  
DB |||||  
QY 5641 GTGTAGCACTTACCAAGTCCAGGAGCTGAGCACTTGTATGATACCCAGATGCCCCACA 5700  
DB |||||  
QY 5701 GCACACTACTGA 5711  
DB |||||  
QY 5701 GCACACTACTGA 5711  
DB |||||

RESULT 5

AAV46468  
ID AAV46468 standard; cDNA; 5711 BP.  
AC AAV46468;  
XX  
XX 18-NOV-1998 (first entry)  
XX Human BRCA1 omi3 polymorphism #4 cDNA.  
XX  
XX BRCA1; omi3; human; breast and ovarian cancer predisposing gene;  
XX polymorphism; susceptibility; anti-oncogene; tumour suppressor;  
XX chromosome 17q; ss.  
XX  
XX Homo sapiens.  
XX  
XX Key Location/Qualifiers  
XX CDS 120..5711  
XX /\*tag= a  
XX /product= "BRCA1 omi3 protein"  
XX variation 3232  
XX /\*tag= b  
XX /note= "This polymorphic variation can be an A or G  
XX nucleotide"

US5750400-A.

12-MAY-1998.

12-FEB-1997; 97US-00798691.

12-FEB-1996; 96US-00598591.

(ONCO-) ONCORMED INC.

Olson SJ, Murphy PD, Zeng B, Alvares CP, Schelter DB, Allen AC;  
Critz BS;

WPI; 1998-296774/26.

BRCA1 omi gene coding sequences - useful for distinguishing between  
polymorphisms and mutation(s) in the screening for disposition to breast  
or ovarian cancer.

Claim 2e; Page; 54pp; English.

This sequence encodes a human BRCA1 (breast and ovarian cancer  
predisposing gene) omi3 gene in which a polymorphic variation occurs at  
nucleotide 3232. This sequence and other polymorphic variations of this  
sequence are useful for the identification of an individual who may or  
may not have an increased susceptibility to breast or ovarian cancer. The  
sequences used identify gene changes which are due to polymorphisms,  
rather than cancer causing mutations. BRCA1 is an anti-oncogene (tumour  
suppressor) which is involved in genetic inheritance of cancers,  
especially breast and ovarian cancer. It is found at human chromosome 17q  
which is known to be linked to cancer susceptibility, especially breast  
cancer. Cells containing a mutation in this gene lose the wild-type  
function of BRCA1 and are more susceptible to cancers. NOTE: This  
sequence does not appear in the specification but has been created from  
the wild type BRCA1 omi3 gene represented in AAV46450

Sequence 5711 BP; 1953 A; 1098 C; 1276 G; 1383 T; 0 U; 1 Other;

Query Match 100.0%; Score 5710.6; DB 2; Length 5711;

Best Local Similarity 100.0%; Pred. NO. 0;

Matches 5710; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTCGCTGAGACTTCTCGGACCCCGCACAGGCTGTGGGGTTTCTCAGATAAATGGGCC 60  
DB |||||  
QY 1 AGCTCGCTGAGACTTCTCGGACCCCGCACAGGCTGTGGGGTTTCTCAGATAAATGGGCC 60  
DB |||||  
QY 61 CCTGCGCTCAGGAGCCCTTCAACCTCTGCTCTGGTAAAGTTCATTGGAACAGAAAGAAA 120  
DB |||||  
QY 61 CCTGCGCTCAGGAGCCCTTCAACCTCTGCTCTGGTAAAGTTCATTGGAACAGAAAGAAA 120  
DB |||||  
QY 121 TGGATTTATCTGCTCTTGGGTTTGAAGAAGTACAAATGTCATTATGCTATGAGAAAA 180  
DB |||||  
QY 121 TGGATTTATCTGCTCTTGGGTTTGAAGAAGTACAAATGTCATTATGCTATGAGAAAA 180  
DB |||||  
QY 181 TCTTAGAGTGTCCATCTGCTCGAGTTGATCAAGGAACTGTCTCCAAAGTGTGACC 240  
DB |||||  
QY 181 TCTTAGAGTGTCCATCTGCTCGAGTTGATCAAGGAACTGTCTCCAAAGTGTGACC 240  
DB |||||  
QY 241 ACATATTTTCAAAATTTTGATCTGTAATCTTCAACCAAGAGAAAGGCGCTTCAAGT 300  
DB |||||  
QY 241 ACATATTTTCAAAATTTTGATCTGTAATCTTCAACCAAGAGAAAGGCGCTTCAAGT 300  
DB |||||  
QY 301 GTCTTTTATGTAAGATGATATTAACCAAAAGAGCCCTACAGAAAGTACAGATTTAGTC 360  
DB |||||  
QY 301 GTCTTTTATGTAAGATGATATTAACCAAAAGAGCCCTACAGAAAGTACAGATTTAGTC 360  
DB |||||  
QY 361 AACTTGTGAAGAGCTATTGAAATCATTTGTCTTTTTCAGCTTGACACAGGTTGAGT 420  
DB |||||  
QY 361 AACTTGTGAAGAGCTATTGAAATCATTTGTCTTTTTCAGCTTGACACAGGTTGAGT 420  
DB |||||  
QY 421 ATGCAAAACAGCTATATTTTGCAGAAAGGAAATTAATCTCTCTGAAACATCTAAAGATG 480  
DB |||||  
QY 421 ATGCAAAACAGCTATATTTTGCAGAAAGGAAATTAATCTCTCTGAAACATCTAAAGATG 480  
DB |||||  
QY 481 AGTTTCTATCATCCAAAGTATGGCTACAGAAACCGTCCAAAGATCTTACAGAGTG 540  
DB |||||  
QY 481 AGTTTCTATCATCCAAAGTATGGCTACAGAAACCGTCCAAAGATCTTACAGAGTG 540  
DB |||||  
QY 541 AACCCGAAATCTTCTCTCAGGAAACAGTCTCAGTGTCCAACTCTTAACCTTGGAA 600  
DB |||||  
QY 541 AACCCGAAATCTTCTCTCAGGAAACAGTCTCAGTGTCCAACTCTTAACCTTGGAA 600  
DB |||||  
QY 601 CTGTGAGAACTCTGAGGACAAAGCAGCGATACAACTCAAAAGACGCTGTCTACATTG 660  
DB |||||  
QY 601 CTGTGAGAACTCTGAGGACAAAGCAGCGATACAACTCAAAAGACGCTGTCTACATTG 660  
DB |||||  
QY 661 AATTGGGATCTGATCTTCTTGAAGATACCGTTAATAGGCAACTTATTGAGTGTGGAG 720  
DB |||||  
QY 661 AATTGGGATCTGATCTTCTTGAAGATACCGTTAATAGGCAACTTATTGAGTGTGGAG 720  
DB |||||  
QY 721 ATCAGAAATGTTACAAATCAACCCCTCAAGAAACCCAGGGATGAAATCAGTTGATCTG 780  
DB |||||

Db 721 ATCAAGAAATGTTACAAATCACCCCTCAAGGAACAGGGATGAATCAATGATTCTG 780  
Qy 781 CAAAAAGCGTCTGTGAAATTTCTGAGACGGATGTAAACAAATCTGAAACATCAATCAAC 840  
Db 781 CAAAAAGCGTCTGTGAAATTTCTGAGACGGATGTAAACAAATCTGAAACATCAATCAAC 840  
Qy 841 CCAGTAATAATGATTTGAACACCACTGAGAGACGCTGAGAGGCGATCCAGAAAAGT 900  
Db 841 CCAGTAATAATGATTTGAACACCACTGAGAGACGCTGAGAGGCGATCCAGAAAAGT 900  
Qy 901 ATCAGGAGTGTCTGTTTCAAACCTTGATGTGAGAGCCATGTGGCAAAATCTCATGCGCA 960  
Db 901 ATCAGGAGTGTCTGTTTCAAACCTTGATGTGAGAGCCATGTGGCAAAATCTCATGCGCA 960  
Qy 961 GCTCAATACAGCATGAGAACAGCAGTCTTATTACTCACTTAAGACAGAGATGAATCTAGAAA 1020  
Db 961 GCTCAATACAGCATGAGAACAGCAGTCTTATTACTCACTTAAGACAGAGATGAATCTAGAAA 1020  
Qy 1021 AGGCTGAATCTGTAATAAAGCAACAGCCTGCTTAGCAGAGGCAACATACAGAT 1080  
Db 1021 AGGCTGAATCTGTAATAAAGCAACAGCCTGCTTAGCAGAGGCAACATACAGAT 1080  
Qy 1081 GGGCTGAGAGTAAGGAACATGTAATGATAGGCGGACTCCAGCACAGAAAAAGGTAG 1140  
Db 1081 GGGCTGAGAGTAAGGAACATGTAATGATAGGCGGACTCCAGCACAGAAAAAGGTAG 1140  
Qy 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAAGTAATGAATGAAGCAAACTGCCATGCT 1200  
Db 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAAGTAATGAATGAAGCAAACTGCCATGCT 1200  
Qy 1201 CAGAGAACTCTAGAGATCTAGAGATGTTCTTGGATTAACACTAAATAGCAGCAATCAGA 1260  
Db 1201 CAGAGAACTCTAGAGATCTAGAGATGTTCTTGGATTAACACTAAATAGCAGCAATCAGA 1260  
Qy 1261 AAGTTAATGAGTGTGTTTCCAGAGATGATGAATCTGTTAGTCTCTGATGACTCACATGATG 1320  
Db 1261 AAGTTAATGAGTGTGTTTCCAGAGATGATGAATCTGTTAGTCTCTGATGACTCACATGATG 1320  
Qy 1321 GGGAGTCTGAATCAAATGCCAAGTAGCTGATGATGATGAGCGTTCTTAATGAGTAGATG 1380  
Db 1321 GGGAGTCTGAATCAAATGCCAAGTAGCTGATGATGATGAGCGTTCTTAATGAGTAGATG 1380  
Qy 1381 AATATTCTGTTCTTCAGAGAAATAGACTTACTGGCCAGTGATCTCATGAGGCTTTAA 1440  
Db 1381 AATATTCTGTTCTTCAGAGAAATAGACTTACTGGCCAGTGATCTCATGAGGCTTTAA 1440  
Qy 1441 TATGTAAGAGTGAAGAGTTCACTCCAAATCAGTAGAGAGTAAATTTGAAGACAAAATAT 1500  
Db 1441 TATGTAAGAGTGAAGAGTTCACTCCAAATCAGTAGAGAGTAAATTTGAAGACAAAATAT 1500  
Qy 1501 TTGGGAAACCTATCGGAAGAGGCAAGCTCCCACTTAAGCCATGTAATCGAAAATC 1560  
Db 1501 TTGGGAAACCTATCGGAAGAGGCAAGCTCCCACTTAAGCCATGTAATCGAAAATC 1560  
Qy 1561 TAATATTAGGAGCAATTTGTTACTGAGCCACAGATAATACAGAGCGTCCCTCCACAAATA 1620  
Db 1561 TAATATTAGGAGCAATTTGTTACTGAGCCACAGATAATACAGAGCGTCCCTCCACAAATA 1620  
Qy 1621 AATTAAGCGTAAAGAGACCTTACATCAGGCTTCACTCTGAGGATTTTATCAAGAAAG 1680  
Db 1621 AATTAAGCGTAAAGAGACCTTACATCAGGCTTCACTCTGAGGATTTTATCAAGAAAG 1680  
Qy 1681 CAGATTTGGCAGTTCAAAAGACTCTCTGAATGATAAATCAGGGAATCAACCAACCGAGC 1740  
Db 1681 CAGATTTGGCAGTTCAAAAGACTCTCTGAATGATAAATCAGGGAATCAACCAACCGAGC 1740  
Qy 1741 AGAATGGTCAAGTGATGAATATTACTAATAGTGGTCAATGAGATAAATAAAGAGTGATT 1800  
Db 1741 AGAATGGTCAAGTGATGAATATTACTAATAGTGGTCAATGAGATAAATAAAGAGTGATT 1800  
Qy 1801 CTATTCAAGATGAGAAAAATCCTTAACCCCAATAGATCACTTCGAAAAAGAAATCTGCTTTCA 1860  
Db 1801 CTATTCAAGATGAGAAAAATCCTTAACCCCAATAGATCACTTCGAAAAAGAAATCTGCTTTCA 1860

Qy 1861 AAACGAAAGCTGAAACCTTATTAAGCAGCAGTATTAAGCAATATGAACTCGAATTAATATCC 1920  
Db 1861 AAACGAAAGCTGAAACCTTATTAAGCAGCAGTATTAAGCAATATGAACTCGAATTAATATCC 1920  
Qy 1921 ACAATTCAAAAGCACCTTAAAGAAATAGGCTGAGGAGGAAGTCTTCTTACCAGGCATATTC 1980  
Db 1921 ACAATTCAAAAGCACCTTAAAGAAATAGGCTGAGGAGGAAGTCTTCTTACCAGGCATATTC 1980  
Qy 1981 ATGCGCTTGAACCTAGTAGTCACTAGAGAAATCTAAGCCCACTGAATTTGCAAT 2040  
Db 1981 ATGCGCTTGAACCTAGTAGTCACTAGAGAAATCTAAGCCCACTGAATTTGCAAT 2040  
Qy 2041 TTGATAGTGTCTTCTAGCAGGTGAAGAGATTAAGAAAGAAAAGTACAACTAATGCCAGTCA 2100  
Db 2041 TTGATAGTGTCTTCTAGCAGGTGAAGAGATTAAGAAAGAAAAGTACAACTAATGCCAGTCA 2100  
Qy 2101 GGCACAGCAGAAACCTTACAACTCATGGAAGGTAAAGAACTCTGCAACTGGAGGCCAAAGAA 2160  
Db 2101 GGCACAGCAGAAACCTTACAACTCATGGAAGGTAAAGAACTCTGCAACTGGAGGCCAAAGAA 2160  
Qy 2161 GTAAACAGCCAAATGACAGACAGTAAAGACATGACAGTGTATCTTTCCAGAGCTGA 2220  
Db 2161 GTAAACAGCCAAATGACAGACAGTAAAGACATGACAGTGTATCTTTCCAGAGCTGA 2220  
Qy 2221 AGTTAAACAATGCACTGCTGTTCTTTTACTAAGTGTTCAAATACAGTGAACCTTAAAGAAAT 2280  
Db 2221 AGTTAAACAATGCACTGCTGTTCTTTTACTAAGTGTTCAAATACAGTGAACCTTAAAGAAAT 2280  
Qy 2281 TTGTCATCTGAGCTTCCAGAGAGAAAGAAAGACAGAAACTTAGAAAAAGTTTAAAGTGT 2340  
Db 2281 TTGTCATCTGAGCTTCCAGAGAGAAAGAAAGACAGAAACTTAGAAAAAGTTTAAAGTGT 2340  
Qy 2341 CTAAATAATCTGAAGACCCCAAGAGTCTCATGTTAAGTGTGAGAAAGGGTTTTCCAAACCTG 2400  
Db 2341 CTAAATAATCTGAAGACCCCAAGAGTCTCATGTTAAGTGTGAGAAAGGGTTTTCCAAACCTG 2400  
Qy 2401 AAAGATCTGAGAGTAGCAGTATTTCTGATCTGCTGATCTGATTAATGSCACTCAGG 2460  
Db 2401 AAAGATCTGAGAGTAGCAGTATTTCTGATCTGCTGATCTGATTAATGSCACTCAGG 2460  
Qy 2461 AAAGATCTGCTGAGTGTAGAGTGTAGCACTCTAGGAGGAGGCAAAACAGAACCAATAAAT 2520  
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Qy 2521 GTGTGAGTCAAGTGTGAGCAATTTGAAACCCCAAGGAGTAAATTTCAATGTTGTTCCAAAG 2580  
Db 2521 GTGTGAGTCAAGTGTGAGCAATTTGAAACCCCAAGGAGTAAATTTCAATGTTGTTCCAAAG 2580  
Qy 2581 AATATAGAAATGACACAGAGGCTTTAAGTATCCATTGGGACATGAGTTAACCAAGTCT 2640  
Db 2581 AATATAGAAATGACACAGAGGCTTTAAGTATCCATTGGGACATGAGTTAACCAAGTCT 2640  
Qy 2641 GGGAAACAGCATAGAAATGGAAGAAAGTGAATCTGATCTGATTTGCAAGATACAT 2700  
Db 2641 GGGAAACAGCATAGAAATGGAAGAAAGTGAATCTGATCTGATTTGCAAGATACAT 2700  
Qy 2701 TCAAGGTTTCAAAGGCCAGTCAATTTGCTCTGTTTCAATCCAGGAAATGCAAGAGG 2760  
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Qy 2761 AATGTGCAACATTTCTCTGCCACTCTGGGTCTTAAAGAAACAAAGTCCAAAGTCACTT 2820  
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Db 2821 TTGAATGTGAACAAAGGAGAAATCAAGGAAAGATGAGTCTTAATATCAAGGCTGTAC 2880  
Qy 2881 AGACAGTGAATATCACTGCGGCTTCTGCTGTTGTTGTCAGAAAGATTAAGCCAGTTGATA 2940  
Db 2881 AGACAGTGAATATCACTGCGGCTTCTGCTGTTGTTGTCAGAAAGATTAAGCCAGTTGATA 2940



QY 2941 ATGCCAAATGTAGTATCAAGAGGCTCTAGGTTTGTCTATCATCTCAGTTCAGAGCA 3000  
DB |||||  
QY 2941 ATGCCAAATGTAGTATCAAGAGGCTCTAGGTTTGTCTATCATCTCAGTTCAGAGCA 3000  
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QY 3001 AGCAAACTGGACTCTATTACTCAAAATAACATGGACTTTTACAAACCCATATCGTATAC 3060  
DB |||||  
QY 3001 AGCAAACTGGACTCTATTACTCAAAATAACATGGACTTTTACAAACCCATATCGTATAC 3060  
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QY 3061 CACCACTTTTCCCATCAAGTCAATTTGTTTAAACTTAAATGTAAAGAAATCTGCTAGAGG 3120  
DB |||||  
QY 3061 CACCACTTTTCCCATCAAGTCAATTTGTTTAAACTTAAATGTAAAGAAATCTGCTAGAGG 3120  
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QY 3121 AAAAATTTGAGGAAATCAATTTGTTTAAACTTAAATGTAAAGAAATCTGCTAGAGG 3180  
DB |||||  
QY 3121 AAAAATTTGAGGAAATCAATTTGTTTAAACTTAAATGTAAAGAAATCTGCTAGAGG 3180  
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QY 3181 GTACAGTGTAGCAATTTAGGCTTAATTAACATTTAGAGAAATCTTTTAAAGGAGCCAGCT 3240  
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QY 3181 GTACAGTGTAGCAATTTAGGCTTAATTAACATTTAGAGAAATCTTTTAAAGGAGCCAGCT 3240  
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QY 3541 ATGCACTCTAGGTTGTTCTGAGCACTGATGACCTGTTAGTATGATGATGATGATGATGATGATG 3600  
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QY 3901 TATCAATTAAGCAATTAAGTGTAGGCTTAAATTAAGTGTAGGCTTAAATTAAGTGTAGGCTTAAAT 3960  
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QY 3961 AGGAACATCACTTAGTGAGGAAACAAATTTCTGCTAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4020  
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DB |||||  
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DB |||||  
QY 4081 CCAAAACAAATGAGGCTCAGTCTGAAAGCCAGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4140  
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QY 4081 CCAAAACAAATGAGGCTCAGTCTGAAAGCCAGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4140  
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QY 4141 TTTTCAGATGATGAAGAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 4200  
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QY 4141 TTTTCAGATGATGAAGAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 4200  
DB |||||  
QY 4201 TGGATTTCAAATTTAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 4260  
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QY 4261 ACTGCTCAGGCTTATCTCTCAGAGTGAATTTTAAACCACTCAGCAGAGGAGTACCAATGC 4320  
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QY 4321 AACATAACCTGATTAAGCTCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 4380  
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QY 4561 CAGATAGTTCTTACAGCTTAAAGAAATTAAGAAATTAAGAAATTAAGAAATTAAGAAATTAAGAAATTAAG 4620  
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QY 4621 GCCCATCATTTAGATGATAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4680  
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QY 4681 ACTACCATCTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 4740  
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QY 4741 AGTCTGGGCCACACAGATTTGACGAAACATCTTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4800  
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QY 4801 CCCCTTACCTGGAAATCTGGAATCAGGCTTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 4860  
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QY 4861 AAGACAGAGG 4920  
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QY 4921 AGCTTCCCAATTTGAAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 4980  
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QY 4981 ATACTCTCTGGGTATTAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATG 5040  
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DB |||||  
QY 5041 CTTTCAACAGG 5100  
DB |||||  
QY 5041 CTTTCAACAGG 5100  
DB |||||  
QY 5101 AATTTATGCTGCTGATCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 5160

DB 5101 AATTATGCTGCTGACAAAGTTGCGCAGAAAACACCATCACTTTAACTAATCTAATTA 5160  
 QY 5161 CTGAGAGACTACTCATGTTGTTATGAAAACAGATGCTGAGTTGTTGTTGAAACGAC 5220  
 DB 5161 CTGAGAGACTACTCATGTTGTTATGAAAACAGATGCTGAGTTGTTGTTGAAACGAC 5220  
 QY 5221 TGAATATTTTCTAGGAATGCGGAGGAAATGGGTAGTTAGCTATTTCTGGGTGACCC 5280  
 DB 5221 TGAATATTTTCTAGGAATGCGGAGGAAATGGGTAGTTAGCTATTTCTGGGTGACCC 5280  
 QY 5281 AGCTATTAAAGAAAATGCTCAATGAGCATGATTTTGAAGTCAGAGAGATGG 5340  
 DB 5281 AGCTATTAAAGAAAATGCTCAATGAGCATGATTTTGAAGTCAGAGAGATGG 5340  
 QY 5341 TCAATGGAGAAACACCAAGGTCCAAAGCGAGCAAGAAATCCAGGACACAAAGATCT 5400  
 DB 5341 TCAATGGAGAAACACCAAGGTCCAAAGCGAGCAAGAAATCCAGGACACAAAGATCT 5400  
 QY 5401 TCAGGGGCTAGAAATGTTGCTATGGCCCTTCAACCAATGCCACAGATCAACTGG 5460  
 DB 5401 TCAGGGGCTAGAAATGTTGCTATGGCCCTTCAACCAATGCCACAGATCAACTGG 5460  
 QY 5461 AATGATGTCAGCTGTTGTTGCTTCTGTTGAGGAGCTTTTCATCATTCACCCCTTG 5520  
 DB 5461 AATGATGTCAGCTGTTGTTGCTTCTGTTGAGGAGCTTTTCATCATTCACCCCTTG 5520  
 QY 5521 GCACAGGTGTCACCAATTTGTTGTTGTCAGCCAGATGCTTGGACAGAGCAATGGCT 5580  
 DB 5521 GCACAGGTGTCACCAATTTGTTGTTGTCAGCCAGATGCTTGGACAGAGCAATGGCT 5580  
 QY 5581 TCCATGCAATTGGGCGAGATGTTGAGGACCTGTTGTCAGCCAGATGCTTGGACAG 5640  
 DB 5581 TCCATGCAATTGGGCGAGATGTTGAGGACCTGTTGTCAGCCAGATGCTTGGACAG 5640  
 QY 5641 GTGTAGCACTCTACCAAGTCCAGGAGCTGGACACCTACTGATACCCAGATGCCCCACA 5700  
 DB 5641 GTGTAGCACTCTACCAAGTCCAGGAGCTGGACACCTACTGATACCCAGATGCCCCACA 5700  
 QY 5701 GCCACTACTGA 5711  
 DB 5701 GCCACTACTGA 5711

## RESULT 6

AAV46465

ID AAV46465 standard; cDNA; 5711 BP.

AC AAV46465;

XX

DT 18-NOV-1998 (first entry)

XX Human BRCA1 omi3 polymorphism #1 cDNA.

DE

XX BRCA1; omi3; human; breast and ovarian cancer predisposing gene;

KW polymorphism; susceptibility; anti-oncogene; tumour suppressor;

KW chromosome 17q; ss.

XX

OS Homo sapiens.

XX

FH Key

FT CDS

FT Location/Qualifiers

FT 120..5711

FT /\*tag= a

FT /product= "BRCA1 omi3 protein"

FT 2201

FT variation

FT /\*tag= b

FT /note= "This polymorphic variation can be a C or T

FT nucleotide"

XX

FN US750400-A.

XX

PD 12-MAY-1998.

XX

PF 12-FEB-1997; 97US-00798691.

XX

XX

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PR

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12-FEB-1996; 96US-00598591.

(ONCO-) ONCORMED INC.

Olson SJ, Murphy PD, Zeng B, Alvares CP, Schelter DB, Allen AC;

Critz BS;

WPI; 1998-296774/26.

BRCA1 omi gene coding sequences - useful for distinguishing between

polymorphisms and mutation(s) in the screening for disposition to breast

or ovarian cancer.

Claim 2e; Page; 54pp; English.

This sequence encodes a human BRCA1 (breast and ovarian cancer

predisposing gene) omi3 gene in which a polymorphic variation occurs at

nucleotide 2201. This sequence and other polymorphic variations of this

sequence are useful for the identification of an individual who may or

may not have an increased susceptibility to breast or ovarian cancer. The

sequences used identify gene changes which are due to polymorphisms,

rather than cancer causing mutations. BRCA1 is an anti-oncogene (tumour

suppressor) which is involved in genetic inheritance of cancers,

especially breast and ovarian cancer. It is found at human chromosome 17q

which is known to be linked to cancer susceptibility, especially breast

cancer. Calls containing a mutation in this gene lose the wild-type

function of BRCA1 and are more susceptible to cancers. NOTE: This

sequence does not appear in the specification but has been created from

the wild type BRCA1 omi3 gene represented in AAV46450

Query Match

Best Local Similarity 100.0%; Score 5710.6; DB 2; Length 5711;

Matches 5710; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTCGCTGAGACTTCTGTGACCCCGCAGCGCTGTGGGTTTCTCAGATACTGGGCC 60

DB 1 AGCTCGCTGAGACTTCTGTGACCCCGCAGCGCTGTGGGTTTCTCAGATACTGGGCC 60

QY 61 CTGCGCTCAGGAGGCGCTTCACTCTGCTCTGGTAAAGTTCAATTGGAACAGAAAGAAA 120

DB 61 CTGCGCTCAGGAGGCGCTTCACTCTGCTCTGGTAAAGTTCAATTGGAACAGAAAGAAA 120

QY 121 TGAATTTATCTGCTCTTTCGGGTTGAAGAGTACAAAATGTCATTATGCTATGCAGAAA 180

DB 121 TGAATTTATCTGCTCTTTCGGGTTGAAGAGTACAAAATGTCATTATGCTATGCAGAAA 180

QY 181 TCTTAGAGTGTCCCATCTGCTGAGTTGATCAAGGAACCTGTCTCCACAAAGTGTGACC 240

DB 181 TCTTAGAGTGTCCCATCTGCTGAGTTGATCAAGGAACCTGTCTCCACAAAGTGTGACC 240

QY 241 ACATATTTTGCATAATTTTGCATGCTGAACTTCTCAACAGAGAAAGGSCCTTACAGT 300

DB 241 ACATATTTTGCATAATTTTGCATGCTGAACTTCTCAACAGAGAAAGGSCCTTACAGT 300

QY 301 GTCCCTTATCTAGAAATGATATACCAAGAGGCGCTTACAGAAAGTACAGATTTTATGTC 360

DB 301 GTCCCTTATCTAGAAATGATATACCAAGAGGCGCTTACAGAAAGTACAGATTTTATGTC 360

QY 361 AACTTGTGTAAGAGCTATTGAAAATCATTTGTGCTTTTTCAGCTTTCAGACAGGTTTGGAGT 420

DB 361 AACTTGTGTAAGAGCTATTGAAAATCATTTGTGCTTTTTCAGCTTTCAGACAGGTTTGGAGT 420

QY 421 ATGCAACAGCTATATTTTGGAAAAGGAAAATTAATCTCTCTGAAACATCTTAAAGATG 480

DB 421 ATGCAACAGCTATATTTTGGAAAAGGAAAATTAATCTCTCTGAAACATCTTAAAGATG 480

QY 481 AAGTTTCTATCATCCAAAGTATGGGCTACAGAAACCGTGCAGAAAGACTTCTACAGAGTG 540

DB 481 AAGTTTCTATCATCCAAAGTATGGGCTACAGAAACCGTGCAGAAAGACTTCTACAGAGTG 540

QY 541 AACCCGAAATCTTCTTCGAGGAAACGAGTCTCAGTGTCCAACTCTCTAACCTTGAA 600  
DB 541 AACCCGAAATCTTCTTCGAGGAAACGAGTCTCAGTGTCCAACTCTCTAACCTTGAA 600  
QY 601 CTGTGAGAACTCTGAGGACAAAGAGCGGATCAAACTCAAAAGACGCTCTGTCTACATG 660  
DB 601 CTGTGAGAACTCTGAGGACAAAGAGCGGATCAAACTCAAAAGACGCTCTGTCTACATG 660  
QY 661 AATTCGGATCTGATCTCTCTGAGGATACCGTTTAATAAGCACTTAATTCGAGTGGGAG 720  
DB 661 AATTCGGATCTGATCTCTCTGAGGATACCGTTTAATAAGCACTTAATTCGAGTGGGAG 720  
QY 721 ATCAAGAAATGTTCACAACTCAACCTCAAGGAACGAGGATGAATCAGTTTGGATCTG 780  
DB 721 ATCAAGAAATGTTCACAACTCAACCTCAAGGAACGAGGATGAATCAGTTTGGATCTG 780  
QY 781 CAAGAAAGCGCTCTGCTGAAATTTCTGAGCGGATGAACAAATCTGAACATCATCAAC 840  
DB 781 CAAGAAAGCGCTCTGCTGAAATTTCTGAGCGGATGAACAAATCTGAACATCATCAAC 840  
QY 841 CCAGTAATAATGATTTGAACCACTCGAGAGCGTGCAGCTGAGAGGCAATCCAGAAAGT 900  
DB 841 CCAGTAATAATGATTTGAACCACTCGAGAGCGTGCAGCTGAGAGGCAATCCAGAAAGT 900  
QY 901 ATCAGGTAGTCTCTGTTCAAACTTGCATTTGGAGCCATTTGGCAAAATCTCATGCCA 960  
DB 901 ATCAGGTAGTCTCTGTTCAAACTTGCATTTGGAGCCATTTGGCAAAATCTCATGCCA 960  
QY 961 GCTCAATTACAGATCAGAACACAGCTTTATTACTCACTAAAGACAGATGAATGAGAAA 1020  
DB 961 GCTCAATTACAGATCAGAACACAGCTTTATTACTCACTAAAGACAGATGAATGAGAAA 1020  
QY 1021 AGGCTGAATCTGTAAATAAGCAACAGCTTGGCTTAGCAGAGGAGCAACATACAGAT 1080  
DB 1021 AGGCTGAATCTGTAAATAAGCAACAGCTTGGCTTAGCAGAGGAGCAACATACAGAT 1080  
QY 1081 GGGCTGGAAGTAAGGAAACATGATAGTGGAGGACTCCAGCACAGAAAGAGTAG 1140  
DB 1081 GGGCTGGAAGTAAGGAAACATGATAGTGGAGGACTCCAGCACAGAAAGAGTAG 1140  
QY 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAGAAATGGAATAGCAGAACTGCCATGCT 1200  
DB 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAGAAATGGAATAGCAGAACTGCCATGCT 1200  
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DB 1261 AAGTTAATGAGTGGTTTTCCAGAAATGATGAATCTGTTAGGTTCTGATGACTCAGATGATG 1320  
QY 1321 GGGAGTCTGAATCAAAATCCAAAGTAGCTGATTTGGAGCTTAAATAGAGTAGATG 1380  
DB 1321 GGGAGTCTGAATCAAAATCCAAAGTAGCTGATTTGGAGCTTAAATAGAGTAGATG 1380  
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DB 1381 AATATTCTGGTTCTTCAGAGAAATAGACTTACTGGCCAGTGATCTCTCATGAGGCTTTAA 1440  
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DB 1441 TATGTAAAGTGAAGAGTTCACTCCAAATCAGTAGAGATTAATTTGAAGCAAAATAT 1500  
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DB 1501 TTGGGAAACCTATCCGAAAGAGGCAAGCTCCCAACTTAAGCCATGATTAAGTCAAAATC 1560  
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DB 1561 TAAATTATAGAGCATTTGTTCTGAGCCACAGATAAATCAAGAGCGTCCCTCAAAATA 1620  
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DB 1621 AATTAAAGCGTAAAGAGGAGACTCATCAGGCTTCTCCTGAGGATTTTATCAAGAAAG 1680  
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QY 1801 CTATTCAAGATGAGAAATAATCTTAAACCAATAGAACTCACTCGAAAAAGAACTCTGCTTCA 1860  
DB 1801 CTATTCAAGATGAGAAATAATCTTAAACCAATAGAACTCACTCGAAAAAGAACTCTGCTTCA 1860  
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QY 1921 ACAATTCAAAAGCACTTAAAAAAGATAGGCTGAGGAGAAAGTCTTCTTACAGGCAATATTC 1980  
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DB 2101 GGCACAGCAGAAACCTTAAACCTATGGAAGTAAAGAACTTAAAGTGGAGCCAAAGA 2160  
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QY 4021 GTGAATTTGAAGACTTTGACTGCAAAATACAAACACCCAGGATCTTTCTTGTGATTTGTTCTT 4080  
DB |||||  
QY 4021 GTGAATTTGAAGACTTTGACTGCAAAATACAAACACCCAGGATCTTTCTTGTGATTTGTTCTT 4080  
DB |||||  
QY 4081 CMAACAAATAGGCAATCAGTCTGAAGACCGAGGAGTTGGTCTGAGTGACAGAGAAATGG 4140  
DB |||||  
QY 4081 CMAACAAATAGGCAATCAGTCTGAAGACCGAGGAGTTGGTCTGAGTGACAGAGAAATGG 4140  
DB |||||  
QY 4141 TTTTCAGATCATCAAGAAAGAGGAAAGGGCTTCGAAAGAAATTAATCAAGAAAGAGCAAGCA 4200  
DB |||||  
QY 4141 TTTTCAGATCATCAAGAAAGAGGAAAGGGCTTCGAAAGAAATTAATCAAGAAAGAGCAAGCA 4200  
DB |||||  
QY 4201 TGGATTCAACTTAGGTGAGGAGGAGCATCTGGGCTGAGAGTGAGGAGGAGGAGGAGGAGGAGG 4260  
DB |||||  
QY 4201 TGGATTCAACTTAGGTGAGGAGGAGCATCTGGGCTGAGAGTGAGGAGGAGGAGGAGGAGGAGG 4260  
DB |||||  
QY 4261 ACTGCTCAGGCTTATCTCTCAGAGTGACATTTTAAACCACTCAGCAGAGGAGTACCATGC 4320  
DB |||||  
QY 4261 ACTGCTCAGGCTTATCTCTCAGAGTGACATTTTAAACCACTCAGCAGAGGAGTACCATGC 4320  
DB |||||  
QY 4321 AACATAAACCCTGATAAGCTTCCAGCAGGAAATGGCTGAACCTAGAGCTGTGTTAGAACAGC 4380  
DB |||||  
QY 4321 AACATAAACCCTGATAAGCTTCCAGCAGGAAATGGCTGAACCTAGAGCTGTGTTAGAACAGC 4380  
DB |||||  
QY 4381 ATGGGAGCCAGCTTCTTAAACAGCTACCTTCCATCATAGTCACTTCTGCGCCCTTGAGG 4440  
DB |||||  
QY 4381 ATGGGAGCCAGCTTCTTAAACAGCTACCTTCCATCATAGTCACTTCTGCGCCCTTGAGG 4440  
DB |||||  
QY 4441 ACCTCGAAATCCAGAACAAAGCAATCAGAAAGGAGGAGTATTAACCTTACAGAAAGGTA 4500  
DB |||||  
QY 4441 ACCTCGAAATCCAGAACAAAGCAATCAGAAAGGAGGAGTATTAACCTTACAGAAAGGTA 4500  
DB |||||  
QY 4501 GTGAATACCTTATAGCCAGGAGTCCAGAGGCTTTCTGCTGACAGGTTGAGGAGGAGGAGGAGG 4560  
DB |||||  
QY 4501 GTGAATACCTTATAGCCAGGAGTCCAGAGGCTTTCTGCTGACAGGTTGAGGAGGAGGAGGAGG 4560  
DB |||||  
QY 4561 CAGATAGTCTTACCAAGTAAAGAAACAGGAGTGAAGAGGCTCATCCCTTCTTAAT 4620  
DB |||||  
QY 4561 CAGATAGTCTTACCAAGTAAAGAAACAGGAGTGAAGAGGCTCATCCCTTCTTAAT 4620  
DB |||||  
QY 4621 GGGCATCATTAGATGATAGGTTGAGTACGACAGTGTCTCTGGGAGTCTTCAAGATAGAA 4680  
DB |||||  
QY 4621 GGGCATCATTAGATGATAGGTTGAGTACGACAGTGTCTCTGGGAGTCTTCAAGATAGAA 4680  
DB |||||  
QY 4681 ACTTACCCATCTCAAGAGGAGGCTCATTAAGGTTGTTGATGTGAGGAGGAGGAGGAGGAGGAGGAGG 4740  
DB |||||

4681 ACTACCCATCTCAAGAGAGCTCATTAAGTTGTTGATGTGGAGGAGCAACAGCTGSAAG 4740  
4741 AGTCTGGGCCACACGATTTGACGAAACATCTTACTTGCAGGCAAGATCTAGAGGAA 4800  
4741 AGTCTGGGCCACACGATTTGACGAAACATCTTACTTGCAGGCAAGATCTAGAGGAA 4800  
4801 CCCCTTACTGGAATCTGGAATCAGCCTCTTCTGTGATGACCTGGAATCTGATCTCTTG 4860  
4801 CCCCTTACTGGAATCTGGAATCAGCCTCTTCTGTGATGACCTGGAATCTGATCTCTTG 4860  
4861 AAGACAGAGCCCGCAGAGTCAGCTCGTGTGTGGCAATACCATCTTCAACCTCTGCATGA 4920  
4861 AAGACAGAGCCCGCAGAGTCAGCTCGTGTGTGGCAATACCATCTTCAACCTCTGCATGA 4920  
4921 AAGTTCCCAATTGAAGTTGAGAAATCTGCCAGGTCAGGTCCTGCTCATACTG 4980  
4921 AAGTTCCCAATTGAAGTTGAGAAATCTGCCAGGTCAGGTCCTGCTCATACTG 4980  
4981 ATACTGCTGGGTATATGCAATGGAAGAAAGTGTGAGCAGGAGAGGAGGAGGAGGAGGAG 5040  
4981 ATACTGCTGGGTATATGCAATGGAAGAAAGTGTGAGCAGGAGAGGAGGAGGAGGAGGAG 5040  
5041 CTTCAACAGAGAGGCTCAACAAAGAAATGTCCATGGTGGTGTCTGGCTGAGCCCGAGAG 5100  
5041 CTTCAACAGAGAGGCTCAACAAAGAAATGTCCATGGTGGTGTCTGGCTGAGCCCGAGAG 5100  
5101 AATTATGCTGTGTACAGTTGTCAGAAACACCAACATCACTTTAACTTAATCTTAATTA 5160  
5101 AATTATGCTGTGTACAGTTGTCAGAAACACCAACATCACTTTAACTTAATCTTAATTA 5160  
5161 CTGAAGAGACTACTCATGTTGTATGAAACAGAGTGTGTGTGTGAAACGAGAC 5220  
5161 CTGAAGAGACTACTCATGTTGTATGAAACAGAGTGTGTGTGTGAAACGAGAC 5220  
5221 TGAATATTTCTAGGAATTCGGGAGGAAATGGGTAGTGTAGCTATTTCTGGGTGACCC 5280  
5221 TGAATATTTCTAGGAATTCGGGAGGAAATGGGTAGTGTAGCTATTTCTGGGTGACCC 5280  
5281 AGTCTATTAAGAAAGAAATGCTGATGAGCATGATTTGAAAGTCAGAGGAGATGAGG 5340  
5281 AGTCTATTAAGAAAGAAATGCTGATGAGCATGATTTGAAAGTCAGAGGAGATGAGG 5340  
5341 TCATGGAAGAAACCAAGAGTCCAAAGCGAGCAAGAGATCCAGGACAGAAAGATCT 5400  
5341 TCATGGAAGAAACCAAGAGTCCAAAGCGAGCAAGAGATCCAGGACAGAAAGATCT 5400  
5401 TCAGGGGCTAGAAATCTGTTGATGAGGCTTTTCCCAACATGCCACAGATCACTGG 5460  
5401 TCAGGGGCTAGAAATCTGTTGATGAGGCTTTTCCCAACATGCCACAGATCACTGG 5460  
5461 AATGATGGTACAGCTGTGTGTGCTTCTGTGTGAGGAGCTTTCAATCACTTCACTTGG 5520  
5461 AATGATGGTACAGCTGTGTGTGCTTCTGTGTGAGGAGCTTTCAATCACTTCACTTGG 5520  
5521 GCAGAGTGTACCCCAATGTTGTTGAGCAGATGCTGAGCAGAGGAGGAGGAGGAGGAG 5580  
5521 GCAGAGTGTACCCCAATGTTGTTGAGCAGATGCTGAGCAGAGGAGGAGGAGGAGGAG 5580  
5581 TCCATGCAATGGGAGATGTTGAGGAGCCTGTGTGTGACCCGAGAGGAGGAGGAGGAGGAG 5640  
5581 TCCATGCAATGGGAGATGTTGAGGAGCCTGTGTGTGACCCGAGAGGAGGAGGAGGAGGAG 5640  
5641 GTGTAGCACTTACAGTGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5700  
5641 GTGTAGCACTTACAGTGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5700  
5701 GCCACTACTGA 5711  
5701 GCCACTACTGA 5711

RESULT 8  
AAV46466

AAV46466 standard; cDNA; 5711 BP.  
AAV46466;  
18-NOV-1998 (first entry)  
Human BRCA1 omi3 polymorphism #2 cDNA.  
BRCA1; omi3; human; breast and ovarian cancer predisposing gene;  
polymorphism; susceptibility; anti-oncogene; tumour suppressor;  
chromosome 17q; ss.  
Homo sapiens.  
Key Location/Qualifiers  
CDS 120..5711  
FT /\*tag= a  
FT /product= "BRCA1 omi3 protein"  
FT variation 2430  
FT /\*tag= b  
FT /note= "This polymorphic variation can be a T or C  
nucleotide"  
US5750400-A.  
12-MAY-1998.  
12-FEB-1997; 97US-00798691.  
12-FEB-1996; 96US-00598591.  
(ONCO-) ONCORMED INC.  
Olson SJ, Murphy PD, Zeng B, Alvares CP, Schelter DB, Allen AC;  
Critz BS;  
WPI; 1998-296774/26.  
BRCA1 omi gene coding sequences - useful for distinguishing between  
polymorphisms and mutation(s) in the screening for disposition to breast  
or ovarian cancer.  
Claim 2e; Page; 54pp; English.  
This sequence encodes a human BRCA1 (breast and ovarian cancer  
predisposing gene) omi3 gene in which a polymorphic variation occurs at  
nucleotide 2430. This sequence and other polymorphic variations of this  
sequence are useful for the identification of an individual who may or  
may not have an increased susceptibility to breast or ovarian cancer. The  
sequences used identify gene changes which are due to polymorphisms,  
rather than cancer causing mutations. BRCA1 is an anti-oncogene (tumour  
suppressor) which is involved in genetic inheritance of cancers,  
especially breast and ovarian cancer. It is found at human chromosome 17q  
which is known to be linked to cancer susceptibility, especially breast  
cancer. Cells containing a mutation in this gene lose the wild-type  
function of BRCA1 and are more susceptible to cancers. NOTE: This  
sequence does not appear in the specification but has been created from  
the wild type BRCA1 omi3 gene represented in AAV46450  
Sequence 5711 BP; 1953 A; 1097 C; 1277 G; 1383 T; 0 U; 1 Other;

Query Match 100.0%; Score 5710.6; DB 2; Length 5711;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 5710; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AGTCTGCTGAGACTTCTCGAGCCCGCAGGCTGTGGGTTTCTCAGATACTGGCC 60  
DB 1 AGTCTGCTGAGACTTCTCGAGCCCGCAGGCTGTGGGTTTCTCAGATACTGGCC 60  
QY 61 CTGCGCTCAGAGGCTTCACTCTGCTCTGGGTAAAGTTTCATTGGACAGAAAGAA 120  
DB 61 CTGCGCTCAGAGGCTTCACTCTGCTCTGGGTAAAGTTTCATTGGACAGAAAGAA 120





Qy	4501	GTGAATACCCCTATTAAGCCAGCAATCCAGAGGCCCTTTCTGCTGACAAGTTTGAGTGTCTG	4561
Db	4501	GTGAATACCCCTATTAAGCCAGCAATCCAGAGGCCCTTTCTGCTGACAAGTTTGAGTGTCTG	4560
Qy	4561	CAGATAGTTCTTACCAGTAAATAAAGAACACAGAGGTGGAAGGTCAATCCCTTCTTAAAT	4620
Db	4561	CAGATAGTTCTTACCAGTAAATAAAGAACACAGAGGTGGAAGGTCAATCCCTTCTTAAAT	4620
Qy	4621	GCCCATCAATTAGATGATAGTGGTACATGCAACAGTTGCTCTGGAGTCTTTCAGATAGAA	4680
Db	4621	GCCCATCAATTAGATGATAGTGGTACATGCAACAGTTGCTCTGGAGTCTTTCAGATAGAA	4680
Qy	4681	ACTTACCCATCTCAAGAGAGCTCAATTAAGTTTGTGATGTGGAGGACACACTGGAG	4740
Db	4681	ACTTACCCATCTCAAGAGAGCTCAATTAAGTTTGTGATGTGGAGGACACACTGGAG	4740
Qy	4741	AGTCTGGGCCACACGATTTGACGGAAACATCTTACTTTGCCAAGGCAAGATCTAGAGGAA	4800
Db	4741	AGTCTGGGCCACACGATTTGACGGAAACATCTTACTTTGCCAAGGCAAGATCTAGAGGAA	4800
Qy	4801	CCCCCTTACCTGGAACTCTGGATCAGCCCTCTCTCTGATGACCCCTGATCTGATCTCTCTG	4860
Db	4801	CCCCCTTACCTGGAACTCTGGATCAGCCCTCTCTCTCTGATGACCCCTGATCTGATCTCTCTG	4860
Qy	4861	AAGACAGAGCCCCAGAGTCACTCGTGTGTGGCAACATACCATCTTCAACCTCTGCCATTTGA	4920
Db	4861	AAGACAGAGCCCCAGAGTCACTCGTGTGTGGCAACATACCATCTTCAACCTCTGCCATTTGA	4920
Qy	4921	AAGTTCCCCAAATTGAAGTTGCAAGATCTGCCAAGGTCAGCTGTGCTCACTACTCTG	4980
Db	4921	AAGTTCCCCAAATTGAAGTTGCAAGATCTGCCAAGGTCAGCTGTGCTCACTACTCTG	4980
Qy	4981	ATACTGCTGGGTATAATTGCAATGAAAGAAAGTGTGACGACGGAGAACCGAAGATTGCACG	5040
Db	4981	ATACTGCTGGGTATAATTGCAATGAAAGAAAGTGTGACGACGGAGAACCGAAGATTGCACG	5040
Qy	5041	CTTCAAACAGAAAGGCTCAAACAAAGAAATGCTCAATGCTGTGCTGACCCCAAG	5100
Db	5041	CTTCAAACAGAAAGGCTCAAACAAAGAAATGCTCAATGCTGTGCTGACCCCAAG	5100
Qy	5101	AATTTATGCTCGTGTACAAGTTTCCAGAAACACACACATCACTTTAACTTAATCTAATTA	5160
Db	5101	AATTTATGCTCGTGTACAAGTTTCCAGAAACACACACATCACTTTAACTTAATCTAATTA	5160
Qy	5161	CTGAAGGAGACTACTCATGTTGTTATGAACACAGATGCTGAGTTTGTGTGGAACGGACAC	5220
Db	5161	CTGAAGGAGACTACTCATGTTGTTATGAACACAGATGCTGAGTTTGTGTGGAACGGACAC	5220
Qy	5221	TGAATATTTTCTAGGAATTTGCGGAGGAAAAATGGGTAGTTAGCTATTTCTGGGTGACCC	5280
Db	5221	TGAATATTTTCTAGGAATTTGCGGAGGAAAAATGGGTAGTTAGCTATTTCTGGGTGACCC	5280
Qy	5281	AGTCTATTAAAGAAAGAAAAATCTGAATCAGCATGAATTTTGAAGTCTCAGAGGAGATGTGG	5340
Db	5281	AGTCTATTAAAGAAAGAAAAATCTGAATCAGCATGAATTTTGAAGTCTCAGAGGAGATGTGG	5340
Qy	5341	TCAATGGAAGAAACCAACAAAGGTCCTGAAGCGACAGAGAAATCCGAGGACAGAAAGATCT	5400
Db	5341	TCAATGGAAGAAACCAACAAAGGTCCTGAAGCGACAGAGAAATCCGAGGACAGAAAGATCT	5400
Qy	5401	TCAGGGGCTTAGAAATCTGTGTGCTATGGGCCCTTTCACCAACATGCCCAAGATCAACTGG	5460
Db	5401	TCAGGGGCTTAGAAATCTGTGTGCTATGGGCCCTTTCACCAACATGCCCAAGATCAACTGG	5460
Qy	5461	AATGGATGGTACAGCTGTGTGGTCTTCTGTGGTGAAGGAGCTTTCATCATTCACCCCTTG	5520
Db	5461	AATGGATGGTACAGCTGTGTGGTCTTCTGTGGTGAAGGAGCTTTCATCATTCACCCCTTG	5520
Qy	5521	GCAACAGTGTCCACCAATTTGTGGTTGTGACGACAGATGCTGCTGACAGAGCAATGGCT	5580
Db	5521	GCAACAGTGTCCACCAATTTGTGGTTGTGACGACAGATGCTGCTGACAGAGCAATGGCT	5580
Qy	5581	TCCATGCAATTGGGCGAGATGTTGAGGACACTGTGGTGTGACCCGAGAGTGGGTCTTGACA	5640

Db	5581	TCCATGCAATTGGGCGAGATGTGTAGGCGACCTGTGTGTGACCCGAGAGTGGGTGTTGGACA	5640
Qy	5641	GTGTAGCACTCTACCACTGTCAGGAGCTGCACACCTTACCTGATACCCAGATCCCCCACA	5700
Db	5641	GTGTAGCACTCTACCACTGTCAGGAGCTGCACACCTTACCTGATACCCAGATCCCCCACA	5700
Qy	5701	GCCCACTACTGA	5711
Db	5701	GCCCACTACTGA	5711
RESULT 9			
AAV46467	AAV46467 standard; cDNA; 5711 BP.		
XX	XX	XX	XX
AC	AAV46467;		
XX	18-NOV-1998	(first entry)	
DT	XX		
XX	XX		
DB	Human BRCA1 omi3 polymorphism #3 cDNA.		
XX	XX		
KW	BRCA1; omi3; human; breast and ovarian cancer predisposing gene;		
KW	polymorphism; susceptibility; anti-oncogene; tumour suppressor;		
KW	chromosome 17q; ss.		
XX	XX		
OS	Homo sapiens.		
XX	XX		
FH	Key	Location/Qualifiers	
FT	CDS	120..5711	
FT	FT	/*tag= a	
FT	FT	/*product= "BRCA1 omi3 protein"	
FT	variation	2731	
FT	FT	/*tag= b	
FT	FT	/*note= "This polymorphic variation can be a C or T nucleotide"	
XX	XX		
PN	US5750400-A.		
XX	XX		
PD	12-MAY-1998.		
XX	XX		
PF	12-FEB-1997;	97US-00798691.	
XX	XX		
PR	12-FEB-1996;	96US-00598591.	
XX	XX		
PA	(ONCO-) ONCORMED INC.		
XX	XX		
PI	Olson SJ, Murphy PD, Zeng B, Alvares CP, Schelter DB, Allen AC;		
PI	Critz BS;		
XX	XX		
DR	WPI; 1998-296774/26.		
XX	XX		
PT	BRCA1 omi gene coding sequences - useful for distinguishing between		
PT	polymorphisms and mutation(s) in the screening for disposition to breast		
PT	or ovarian cancer.		
XX	XX		
PS	Claim 2e; Page; 54pp; English.		
XX	XX		
CC	This sequence encodes a human BRCA1 (breast and ovarian cancer predisposing gene) omi3 gene in which a polymorphic variation occurs at nucleotide 2731. This sequence and other polymorphic variations of this sequence are useful for the identification of an individual who may or may not have an increased susceptibility to breast or ovarian cancer. The sequences used identify gene changes which are due to polymorphisms, rather than cancer causing mutations. BRCA1 is an anti-oncogene (tumour suppressor) which is involved in genetic inheritance of cancers, especially breast and ovarian cancer. It is found at human chromosome 17q which is known to be linked to cancer susceptibility, especially breast cancer. Cells containing a mutation in this gene lose the wild-type function of BRCA1 and are more susceptible to cancers. NOTE: This sequence does not appear in the specification but has been created from the wild type BRCA1 omi3 gene represented in AAV46450		
XX	XX		

SQ Sequence 5711 BP; 1953 A; 1098 C; 1277 G; 1382 T; 0 U; 1 Other;									
Query Match 100.0%; Score 5710.6; DB 2; Length 5711;									
Best Local Similarity 100.0%; Pred. No. 0;									
Matches 5710; Conservative 1; Mismatches 0; Indels 0; Gaps 0;									
Qy	1	AGCTGCGTGAAGCTCTCTGACCCCGACACCGAGCTGTGGGGTTCTTCAGATTAACCTGGGCC	60						
Db	1	AGCTGCGTGAAGCTCTCTGACCCCGACACCGAGCTGTGGGGTTCTTCAGATTAACCTGGGCC	60						
Qy	61	CCTGGCGTCAGAGGCGCTTCAACCCCTCTGCTCTGGGTAAAGTTCAATTGGAAACAGAAAGAAA	120						
Db	61	CCTGGCGTCAGAGGCGCTTCAACCCCTCTGCTCTGGGTAAAGTTCAATTGGAAACAGAAAGAAA	120						
Qy	121	TGGAATTAATCTGCTCTTCGCGTTGAGAGAGTACAAAATGTCAATTAATCTGATGAGAGAAA	180						
Db	121	TGGAATTAATCTGCTCTTCGCGTTGAGAGAGTACAAAATGTCAATTAATCTGATGAGAGAAA	180						
Qy	181	TCCTTAGAGTGTCCCATCTGCTGAGTGTGATCAAGGACCTGTCTCCACAAAGTGTGACC	240						
Db	181	TCCTTAGAGTGTCCCATCTGCTGAGTGTGATCAAGGACCTGTCTCCACAAAGTGTGACC	240						
Qy	241	ACATATTTTGCATTTTGTGATGCTGAAACCTTCTCAACAGAGAGGGGCTTTCACAGT	300						
Db	241	ACATATTTTGCATTTTGTGATGCTGAAACCTTCTCAACAGAGAGGGGCTTTCACAGT	300						
Qy	301	GTCCCTTTATGTAAGATGATATACCAAAAGGAGCCTACAGAAAGTACGAGATTTAGTC	360						
Db	301	GTCCCTTTATGTAAGATGATATACCAAAAGGAGCCTACAGAAAGTACGAGATTTAGTC	360						
Qy	361	AACCTGTGTGAAGAGCTATGGAATTCATTTGTGCTTTTCAGCTTTGACACAGGTTTGGAGT	420						
Db	361	AACCTGTGTGAAGAGCTATGGAATTCATTTGTGCTTTTCAGCTTTGACACAGGTTTGGAGT	420						
Qy	421	ATGCAGACAGCTATTAATTTTGCAGAAAGGAGAAATTAATCTCTGACATCTTAAAGATG	480						
Db	421	ATGCAGACAGCTATTAATTTTGCAGAAAGGAGAAATTAATCTCTGACATCTTAAAGATG	480						
Qy	481	AAGTTTCTATCATCCAAAGTATGGCTACAGAAACCGTGCCAAAGAGCTTCTACAGAGTG	540						
Db	481	AAGTTTCTATCATCCAAAGTATGGCTACAGAAACCGTGCCAAAGAGCTTCTACAGAGTG	540						
Qy	541	AACCCGAAATCTTCTCTGAGGAAACCACTCTCAGTGTCCAACTCTTAAACCTTGGAA	600						
Db	541	AACCCGAAATCTTCTCTGAGGAAACCACTCTCAGTGTCCAACTCTTAAACCTTGGAA	600						
Qy	601	CTGTGAGAACTCTGAGGACAAAGCAGCGGATACAACTTCAAGAGCTGTCTTACATTG	660						
Db	601	CTGTGAGAACTCTGAGGACAAAGCAGCGGATACAACTTCAAGAGCTGTCTTACATTG	660						
Qy	661	AATTGGGATCTGATTTCTTCAAGATACCGTTAATAAGGCAACTTATTGGCAGTGTGGAG	720						
Db	661	AATTGGGATCTGATTTCTTCAAGATACCGTTAATAAGGCAACTTATTGGCAGTGTGGAG	720						
Qy	721	ATCAAGAAATGTTTCAATCAACCTCAGGAAACAGGATGAATCAATGTTGATTTCTG	780						
Db	721	ATCAAGAAATGTTTCAATCAACCTCAGGAAACAGGATGAATCAATGTTGATTTCTG	780						
Qy	781	CAAAAAGGCTGCTTGTGAAATTTCTGAGACGGATGTAAACAAATACTGMACTCATCAAC	840						
Db	781	CAAAAAGGCTGCTTGTGAAATTTCTGAGACGGATGTAAACAAATACTGMACTCATCAAC	840						
Qy	841	CCAGTAATATGATTTGAAACCACTGAGAAAGCGTGACGTGAGAGGATCCAGAAAAGT	900						
Db	841	CCAGTAATATGATTTGAAACCACTGAGAAAGCGTGACGTGAGAGGATCCAGAAAAGT	900						
Qy	901	ATCAGGGTGTGTTTCTTCAAACTTGATGTGGAGCCATGTGGCACAATACTCATGCCA	960						
Db	901	ATCAGGGTGTGTTTCTTCAAACTTGATGTGGAGCCATGTGGCACAATACTCATGCCA	960						
Qy	961	GCTCATTTACAGCATGAGAAACAGAGTTTATTTACTCACTPAAAGACAGATGATGTAGAA	1020						
Db	961	GCTCATTTACAGCATGAGAAACAGAGTTTATTTACTCACTTAAAGACAGATGATGTAGAA	1020						
Qy	1021	AGGCTGAATTTCTGTAAATAAAGCAACAGCCTGGCTTTAGCAAGGAGCCAAATAACAGAT	1080						
Db	1021	AGGCTGAATTTCTGTAAATAAAGCAACAGCCTGGCTTTAGCAAGGAGCCAAATAACAGAT	1080						
Qy	1081	GGGCTGGAAGTAAAGAAACATGTAAATGATAGGGGAGACTCCACGACAGAAAAGAGTAG	1140						
Db	1081	GGGCTGGAAGTAAAGAAACATGTAAATGATAGGGGAGACTCCACGACAGAAAAGAGTAG	1140						
Qy	1141	ATCTGAATCTGATCCCTCTGTGTGAGAGAAAAGATGGAATAAGCAGAAAACCTGCCATGCT	1200						
Db	1141	ATCTGAATCTGATCCCTCTGTGTGAGAGAAAAGATGGAATAAGCAGAAAACCTGCCATGCT	1200						
Qy	1201	CAGAGAACTCTAGAGATACCTGAAGATGTTCCTTTGGATTAACAATAAGCAGCAATTCAGA	1260						
Db	1201	CAGAGAACTCTAGAGATACCTGAAGATGTTCCTTTGGATTAACAATAAGCAGCAATTCAGA	1260						
Qy	1261	AAGTTAATGAGTGGTTTTCAGAAAGTGTGAACTGTAGTCTGTGATGACTCACATGATG	1320						
Db	1261	AAGTTAATGAGTGGTTTTCAGAAAGTGTGAACTGTAGTCTGTGATGACTCACATGATG	1320						
Qy	1321	GGGAGTCTGAATCAAAATGCAAGTGTGATGTATTGGACGTTCTAAATGAGGTAGATG	1380						
Db	1321	GGGAGTCTGAATCAAAATGCAAGTGTGATGTATTGGACGTTCTAAATGAGGTAGATG	1380						
Qy	1381	AATATTCTGCTCTCTCAGAGAAATAGACTTACTGCGCAGTGATCTCTATGAGGCTTTAA	1440						
Db	1381	AATATTCTGCTCTCTCAGAGAAATAGACTTACTGCGCAGTGATCTCTATGAGGCTTTAA	1440						
Qy	1441	TATGTAAGAGTGAAGAGTTCACTCCAAATCAGTAGAGATTAATATTGGAAGACAAAATAT	1500						
Db	1441	TATGTAAGAGTGAAGAGTTCACTCCAAATCAGTAGAGATTAATATTGGAAGACAAAATAT	1500						
Qy	1501	TTGGGAAACCTTATCGGAGAGGAGCGCTCCCAACTTAAGCCATGTAACCTGAAATC	1560						
Db	1501	TTGGGAAACCTTATCGGAGAGGAGCGCGCTCCCAACTTAAGCCATGTAACCTGAAATC	1560						
Qy	1561	TAATATTAGAGCATTTGTTTACTGAGCCACAGATAATACAAGAGCGTCCCTCACAAATA	1620						
Db	1561	TAATATTAGAGCATTTGTTTACTGAGCCACAGATAATACAAGAGCGTCCCTCACAAATA	1620						
Qy	1621	AATTAAAGCGTAAAGAGACCTACATCAGGCGCTTCTCTGAGGATTTTATCAAGAAAG	1680						
Db	1621	AATTAAAGCGTAAAGAGACCTACATCAGGCGCTTCTCTGAGGATTTTATCAAGAAAG	1680						
Qy	1681	CAGATTGGCAGTTCAAAAGACTCCTGAAATGATAATCAGGAACTTAACCAACCGAGC	1740						
Db	1681	CAGATTGGCAGTTCAAAAGACTCCTGAAATGATAATCAGGAACTTAACCAACCGAGC	1740						
Qy	1741	AGAATGGTCAAGTGTGAATATTACTTAATAGTGGTCAATGAGAAATAAAAGGTTGAT	1800						
Db	1741	AGAATGGTCAAGTGTGAATATTACTTAATAGTGGTCAATGAGAAATAAAAGGTTGAT	1800						
Qy	1801	CTATTCCAGATGAGAAAATCCCTAACCCATAGAACTCCTCGAAAAGAGATCTGCTTTCA	1860						
Db	1801	CTATTCCAGATGAGAAAATCCCTAACCCATAGAACTCCTCGAAAAGAGATCTGCTTTCA	1860						
Qy	1861	AAAACGAAAGCTGAACCTTAAAGCAGCAGTATAAGCAATATGGAACCTGAAATTAATCC	1920						
Db	1861	AAAACGAAAGCTGAACCTTAAAGCAGCAGTATAAGCAATATGGAACCTGAAATTAATCC	1920						
Qy	1921	ACAATTTCAAAGCACCTTAAAGAAATAGGCTGAGGAGGAGTCTTCTACAGGCAATTC	1980						
Db	1921	ACAATTTCAAAGCACCTTAAAGAAATAGGCTGAGGAGGAGTCTTCTACAGGCAATTC	1980						
Qy	1981	ATCGGCTTGAATCTAGTAGTCAAGTAAATCTAAGCCACCTAATTTGCTGAATTTGAAA	2040						
Db	1981	ATCGGCTTGAATCTAGTAGTCAAGTAAATCTAAGCCACCTAATTTGCTGAATTTGAAA	2040						
Qy	2041	TTGATAGTGTCTTACGAGTGAAGAGATTAAGAAAAAAGTACACCAANTGCCAGTCA	2100						
Db	2041	TTGATAGTGTCTTACGAGTGAAGAGATTAAGAAAAAAGTACACCAANTGCCAGTCA	2100						





Db 4261 ACTGCTAGGGCTATCTCTCAGAGTGACATTTTAAACCACTCAGCAGAGGGATACCATGC 4320  
Qy 4321 AACATAACCTGATAAAGCTCCAGCAGGAAATGGCTGAACCTAGAAAGCTGTGTAGAAACAGC 4380  
Db 4321 AACATAACCTGATAAAGCTCCAGCAGGAAATGGCTGAACCTAGAAAGCTGTGTAGAAACAGC 4380  
Qy 4381 ATGGGAGCCAGCTCTTAACAGCTACCTTCCATCATTAAGTGACTCTTCTGCCCCCTGAGG 4440  
Db 4381 ATGGGAGCCAGCTCTTAACAGCTACCTTCCATCATTAAGTGACTCTTCTGCCCCCTGAGG 4440  
Qy 4441 ACCTGCGAATPCCAGAACAAAGCAGCATCAGAAAAAGCAGTATTAACTTCAAGAAAAAGTA 4500  
Db 4441 ACCTGCGAATPCCAGAACAAAGCAGCATCAGAAAAAGCAGTATTAACTTCAAGAAAAAGTA 4500  
Qy 4501 GTGAATACCTTAAAGCCAGATCCAGAGGCTTCTGCTGACAAAGCTTTGAGGTCTCG 4560  
Db 4501 GTGAATACCTTAAAGCCAGATCCAGAGGCTTCTGCTGACAAAGCTTTGAGGTCTCG 4560  
Qy 4561 CAGATAGTCTTACCAAGTAAATAAAGAACCCAGAGTGGAAAGTCTATCCCTTCTAAAT 4620  
Db 4561 CAGATAGTCTTACCAAGTAAATAAAGAACCCAGAGTGGAAAGTCTATCCCTTCTAAAT 4620  
Qy 4621 GCCCATCATTAGATGATGGTGTACATGACAGTGTCTCTGGAGTCTTCAAGATAGAA 4680  
Db 4621 GCCCATCATTAGATGATGGTGTACATGACAGTGTCTCTGGAGTCTTCAAGATAGAA 4680  
Qy 4681 ACTACCCATCTCAAGAGAGCTCATTAAGGTTGTTGATGTGGAGAGCAACAGCTGGAAG 4740  
Db 4681 ACTACCCATCTCAAGAGAGCTCATTAAGGTTGTTGATGTGGAGAGCAACAGCTGGAAG 4740  
Qy 4741 AGTCTGGGCCACACGATTGAGGAAACATCTTACTTCCCAAGCAAGATCTAGAGGAA 4800  
Db 4741 AGTCTGGGCCACACGATTGAGGAAACATCTTACTTCCCAAGCAAGATCTAGAGGAA 4800  
Qy 4801 CCCCTTACCTGGAATCTGGAATCAGCTCTCTCTGATGACCTGGAATCTGATCTCTCTG 4860  
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Qy 4861 AAGACAGAGCCCAAGAGTCACTGCTGTGGCAACATACCATCTTCAACCTCTGCAITGA 4920  
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Qy 4921 AAGTTCCTCCATCTGAAGTTGCAGAACTCTGCCAGGCTCAGCTGCTGCTCATCTACTG 4980  
Db 4921 AAGTTCCTCCATCTGAAGTTGCAGAACTCTGCCAGGCTCAGCTGCTGCTCATCTACTG 4980  
Qy 4981 ATACTGCTGGGTATAATGCAATGGAAGAAAGTGTGACGAGGAGAACCCAGAAATTCACAG 5040  
Db 4981 ATACTGCTGGGTATAATGCAATGGAAGAAAGTGTGACGAGGAGAACCCAGAAATTCACAG 5040  
Qy 5041 CTTCAACAGAAAGGGTCAACAAAGAAATGTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5100  
Db 5041 CTTCAACAGAAAGGGTCAACAAAGAAATGTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5100  
Qy 5101 AATTATGCTGCTGTACAGTTTCCAGAAAAACACACATCACTTTAACTAACTTAATTA 5160  
Db 5101 AATTATGCTGCTGTACAGTTTCCAGAAAAACACACATCACTTTAACTAACTTAATTA 5160  
Qy 5161 CTGAAGAGACTACTCATGTTTATGAATAAAGAGATGCTGAGTTTGTGTGAAACGAGAC 5220  
Db 5161 CTGAAGAGACTACTCATGTTTATGAATAAAGAGATGCTGAGTTTGTGTGAAACGAGAC 5220  
Qy 5221 TGAATATTTCTAGGAATTCGGGAGGAAATGGGTAGTTAGCTATTTCTGCTGCTGCTGCTG 5280  
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Qy 5281 AGTCTAATAAGAAAGAAAAATCTGAATGAGCATGATTTTGAAGTCAGAGGAGATGTGG 5340  
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Qy 5341 TCAATGGAAGAACCAACCAAGGTCCTCAAGCGAGCAAGAGATCCAGGACAGAAAGTCT 5400  
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Qy 5401 TCAGGGGGCTAGAAATCTGTTGCTATGGGCCCTTCCAAACATGCCCAAGATCAACTGG 5460  
Db 5401 TCAGGGGGCTAGAAATCTGTTGCTATGGGCCCTTCCAAACATGCCCAAGATCAACTGG 5460  
Qy 5461 AATGGATGGTACAGCTGTGTGGTCTTCTGTGTGAAGGAGCTTTTCATCATTCACCCCTTG 5520  
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Qy 5521 GCACAGGTGTCCACCAATTTGTTGTCAGCCAGCATGCTGTGAGAGCAAGAGCAANTGGCT 5580  
Db 5521 GCACAGGTGTCCACCAATTTGTTGTCAGCCAGCATGCTGTGAGAGCAAGAGCAANTGGCT 5580  
Qy 5581 TCCATGCAATTTGGGCGAGATGTGTGAGGCACTCTGTGTGACCCGAGAGTGGTGTGGACA 5640  
Db 5581 TCCATGCAATTTGGGCGAGATGTGTGAGGCACTCTGTGTGACCCGAGAGTGGTGTGGACA 5640  
Qy 5641 GTGTAGCACTCTACCAAGTCCAGGAGCTGAGACCTTACTGTATACCCAGATCCCCACA 5700  
Db 5641 GTGTAGCACTCTACCAAGTCCAGGAGCTGAGACCTTACTGTATACCCAGATCCCCACA 5700  
Qy 5701 GCCCACTACTGA 5711  
Db 5701 GCCCACTACTGA 5711

## RESULT 10

AAV46469

ID AAV46469 standard; cDNA; 5711 BP.

XX AAV46469;

AC XX

DT 18-NOV-1998 (first entry)

XX Human BRCA1 omi3 polymorphism #5 cDNA.

DE BRCA1; omi2; human; breast and ovarian cancer predisposing gene;

XX polymorphism; susceptibility; anti-oncogene; tumour suppressor;

KW chromosome 17q; ss.

XX Homo sapiens.

XX

PH Key

CDS Location/Qualifiers

FT 120..5711

FT /\*tag= a

FT /product= "BRCA1 omi3 protein"

FT variation 3667

FT /\*tag= b

FT /note= "This polymorphic variation can be an A or G

FT nucleotide"

XX

XX US5750400-A.

XX 12-MAY-1998.

XX 12-FEB-1997; 97US-00798691.

XX 12-FEB-1996; 96US-00598591.

XX (ONCO-) ONCORMED INC.

XX Olson SJ, Murphy PD, Zeng B, Alvares CP, Schelter DB, Allen AC;

XX Critz BS,

XX WPI; 1998-296774/36.

XX

XX BRCA1 omi gene coding sequences - useful for distinguishing between

XX polymorphisms and mutation(s) in the screening for disposition to breast

XX or ovarian cancer.

XX

XX Claim 2e; Page; 54pp; English.

XX This sequence encodes a human BRCA1 (breast and ovarian cancer

XX

CC predisposing gene) omi3 gene in which a polymorphic variation occurs at  
CC nucleotide 3657. This sequence and other polymorphic variations of this  
CC sequence are useful for the identification of an individual who may or  
CC may not have an increased susceptibility to breast or ovarian cancer. The  
CC sequences used identify gene changes which are due to polymorphisms,  
CC rather than cancer causing mutations. BRCA1 is an anti-oncogene (tumour  
CC suppressor) which is involved in genetic inheritance of cancers,  
CC especially breast and ovarian cancer. It is found at human chromosome 17q  
CC which is known to be linked to cancer susceptibility, especially breast  
CC cancer. Cells containing a mutation in this gene lose the wild-type  
CC function of BRCA1 and are more susceptible to cancers. NOTE: This  
CC sequence does not appear in the specification but has been created from  
CC the wild type BRCA1 omi3 gene represented in AAV46450  
XX

SQ Sequence 5711 BP; 1953 A; 1098 C; 1276 G; 1383 T; 0 U; 1 Other;

Query Match 100.0%; Score 5710.6; DB 2; Length 5711;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 5710; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY	1	AGCTCGCTGAGACTTCCTGGACCCCGCACCGGCTGGGGTCTCAGATAACTGGGCC	60
DB	1	AGCTCGCTGAGACTTCCTGGACCCCGCACCGGCTGGGGTCTCAGATAACTGGGCC	60
QY	61	CCTGGGCTCAGAGGCTTCACCTCTGCTCTGGGTAAAGTTCAATTGGAAACAGAAAGAAA	120
DB	61	CCTGGGCTCAGAGGCTTCACCTCTGCTCTGGGTAAAGTTCAATTGGAAACAGAAAGAAA	120
QY	121	TGGATTTATCTGCTCTGGGTTGAAGATACAAAGTCTATTAAGTCTATGAGAAA	180
DB	121	TGGATTTATCTGCTCTGGGTTGAAGATACAAAGTCTATTAAGTCTATGAGAAA	180
QY	181	TCTTAGAGTGTCCCATCTGTCTGGAGTTGATCAAGAACCTGTCTCCACAAAGTGTGACC	240
DB	181	TCTTAGAGTGTCCCATCTGTCTGGAGTTGATCAAGAACCTGTCTCCACAAAGTGTGACC	240
QY	241	ACATATTTTGCMAATTTTGATGCTGAAACTTCTCAACAGAGAAAGGGCTTCACAGT	300
DB	241	ACATATTTTGCMAATTTTGATGCTGAAACTTCTCAACAGAGAAAGGGCTTCACAGT	300
QY	301	GTCTTTTATGTAAGATGATATAACAAAGAGGCTACAGAAAGTACGAGATTTAGTC	360
DB	301	GTCTTTTATGTAAGATGATATAACAAAGAGGCTACAGAAAGTACGAGATTTAGTC	360
QY	361	AATTTGTTGAAGAGCTATGAAATCATTTGTGCTTTTTCAGCTTGACACAGTTTGAGT	420
DB	361	AATTTGTTGAAGAGCTATGAAATCATTTGTGCTTTTTCAGCTTGACACAGTTTGAGT	420
QY	421	ATGCAACAGCTATTAATTTTGCMAAAGAGAAATAACTCTCTGAAACATCTAAAGATG	480
DB	421	ATGCAACAGCTATTAATTTTGCMAAAGAGAAATAACTCTCTGAAACATCTAAAGATG	480
QY	481	AAGTTTCTATCATCCAAAGTATGGGCTACAGAAACCGTGCCAAAGAGCTTCTACAGATG	540
DB	481	AAGTTTCTATCATCCAAAGTATGGGCTACAGAAACCGTGCCAAAGAGCTTCTACAGATG	540
QY	541	RACCCGAATCTTCTTGGAGAAACCGCTCTCAGTGTCCACTCTACCTTGAA	600
DB	541	RACCCGAATCTTCTTGGAGAAACCGCTCTCAGTGTCCACTCTACCTTGAA	600
QY	601	CTGTGAGAACTCTGAGGACAAAGCAGCGGATACAACTCAAAAGACGTCCTACATTG	660
DB	601	CTGTGAGAACTCTGAGGACAAAGCAGCGGATACAACTCAAAAGACGTCCTACATTG	660
QY	661	AATGGGATCTGATTTCTGAGATACGGTTATTAAGGCACTTATTCGAGTGGAG	720
DB	661	AATGGGATCTGATTTCTGAGATACGGTTATTAAGGCACTTATTCGAGTGGAG	720
QY	721	ATCAAGAAATTTTACAAATCAACCTCAAGGAAACAGGGATGAATCAGTTTGGATCTG	780
DB	721	ATCAAGAAATTTTACAAATCAACCTCAAGGAAACAGGGATGAATCAGTTTGGATCTG	780
QY	781	CAAAAAGGCTGCTTGTGAAATTTTCTGAGACGGATGTAACTACTGAAATCAATCAAC	840

DB	781	CAAAAAGGCTGCTTGTGAAATTTTCTGAGACGGATGTAACTACTGAAATCATCATCAAC	840
QY	841	CCAGTAATATGATTTTGAACACCACTGAGAGCGTGCAGCTGAGAGCGATCCAGAAAGT	900
DB	841	CCAGTAATATGATTTTGAACACCACTGAGAGCGTGCAGCTGAGAGCGATCCAGAAAGT	900
QY	901	ATCAGGGTAGTTCCTGTTTCAAACTTCCATCTGAGCGCATGTGGCAAAAATCTCATGCCA	960
DB	901	ATCAGGGTAGTTCCTGTTTCAAACTTCCATCTGAGCGCATGTGGCAAAAATCTCATGCCA	960
QY	961	GCTCATTACAGCAGTGAACAGCAGTTTATTACTACTAAAGACAGAAATGAATGTAGAAA	1020
DB	961	GCTCATTACAGCAGTGAACAGCAGTTTATTACTACTAAAGACAGAAATGAATGTAGAAA	1020
QY	1021	AGCTGATTTCTCTAATTAAGCAACACCGCTGTAGCAAGAGGCCAATACATACAGAT	1080
DB	1021	AGCTGATTTCTCTAATTAAGCAACACCGCTGTAGCAAGAGGCCAATACATACAGAT	1080
QY	1081	GGCTCGAACTAAAGAAACATGTAAATGATAGGGGACTCCACGACAGAAAAAAGGTAG	1140
DB	1081	GGCTCGAACTAAAGAAACATGTAAATGATAGGGGACTCCACGACAGAAAAAAGGTAG	1140
QY	1141	ATCTGAATGCTGATCCCTCTGTGTGAGAAAGAAATGGATTAAGCAAGAACTGCCATCT	1200
DB	1141	ATCTGAATGCTGATCCCTCTGTGTGAGAAAGAAATGGATTAAGCAAGAACTGCCATCT	1200
QY	1201	CAGAGATCTTAGAGTACTGAAAGATGTTCTCTTGGATAACACTAAATAGCAGATTGAGA	1260
DB	1201	CAGAGATCTTAGAGTACTGAAAGATGTTCTCTTGGATAACACTAAATAGCAGATTGAGA	1260
QY	1261	AAGTTAATGAGTGGTTTTCCAGAAATGATGAATCTGTGTAGTTCTGATCTCATGATG	1320
DB	1261	AAGTTAATGAGTGGTTTTCCAGAAATGATGAATCTGTGTAGTTCTGATCTCATGATG	1320
QY	1321	GGGAGTCTGAATCAAAATGCCAAAGTAGTGTATTTGGACGTTCTAAATGAGGTAGATG	1380
DB	1321	GGGAGTCTGAATCAAAATGCCAAAGTAGTGTATTTGGACGTTCTAAATGAGGTAGATG	1380
QY	1381	AATAFTCTGCTTTCTCAGAGAAATAGACTTACTTGCCAGTGTATCTCATGAGGCTTTAA	1440
DB	1381	AATAFTCTGCTTTCTCAGAGAAATAGACTTACTTGCCAGTGTATCTCATGAGGCTTTAA	1440
QY	1441	TATGTAAAGTGAAGAGTTTCACTCCAAATCAGTAGAGTATATTTGAAGACAAATAT	1500
DB	1441	TATGTAAAGTGAAGAGTTTCACTCCAAATCAGTAGAGTATATTTGAAGACAAATAT	1500
QY	1501	TTGGAAAACTTATCGGAGAGGCGAAGCCTCCCAACTTTAAGCCATGTAACTGAAAAATC	1560
DB	1501	TTGGAAAACTTATCGGAGAGGCGAAGCCTCCCAACTTTAAGCCATGTAACTGAAAAATC	1560
QY	1561	TAAATATAGGAGCATTTGTTTACTGAGCCACAGATATATCAAGAGCGTCCCTCACAATA	1620
DB	1561	TAAATATAGGAGCATTTGTTTACTGAGCCACAGATATATCAAGAGCGTCCCTCACAATA	1620
QY	1621	AATTAAGCGTAAAGAGGACCTACATCAGGCGCTTCTATCTGAGGATTTTATCAAGAAAG	1680
DB	1621	AATTAAGCGTAAAGAGGACCTACATCAGGCGCTTCTATCTGAGGATTTTATCAAGAAAG	1680
QY	1681	CAGATTTGGCAGTTTCAAAAAGTCTCTGAATATGATAATCAGGGAATTAACCAACCGGAGC	1740
DB	1681	CAGATTTGGCAGTTTCAAAAAGTCTCTGAATATGATAATCAGGGAATTAACCAACCGGAGC	1740
QY	1741	AGATGCTCAAGTGTGATTAATTAATAGTGTCTATGAGTAATAAACAAGAGGTGATT	1800
DB	1741	AGATGCTCAAGTGTGATTAATTAATAGTGTCTATGAGTAATAAACAAGAGGTGATT	1800
QY	1801	CTATTTCAGATGAGAAAAATCTTAACCAATAGAAATCACTCGMAAAGAAATCTGCTTCA	1860
DB	1801	CTATTTCAGATGAGAAAAATCTTAACCAATAGAAATCACTCGMAAAGAAATCTGCTTCA	1860
QY	1861	AAACGAAGCTGACCTTATTAAGCAGGATATAGCAATATGGAACTCGAATTAATATCC	1920

1861 AAAACGAAGCTGAACTATAGCAGCAGTATATAGCAATATATGGAACCTCGAATTAATATATCC 1920  
1921 ACAATTTAAAGCAGCTTAAAGAAATAGCTGAGGAGGAGTCTTCTACCGAGCATATTC 1980  
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2461 AAAAGTATCTGTTACTGGAAGTTAGCACTCTAGGAGGCAAAACAGAACCAATAAT 2520  
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DB 4081 CCAACAAATGAGGATCAGTCTGAAGCCAGGAGTTGGTCTGAGTGACAGGAATTGG 4140  
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QY 4441 ACCTGCGAAATCCAGAAACAGCAATCAGAAAAGCAGTATTAACTTCAAGAAAAGTA 4500  
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DB 4561 CAGATAGTTCTACAGTAAAAATAAAGAACCGAGAGTGAAGGTCTATCCCTTCTAAAT 4620  
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DB 4621 GCCCATCATATGATAGTGGTATGATGATGATGATGATGATGATGATGATGATGATGATG 4680  
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DB 4741 AGTCTGGGCGCACAGATTTGAGGAAACATCTTCTGCTGCAAGGAGCAAGATCTAGAGGAA 4800  
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DB 5101 AATTATTGCTGCTGATCAAGTTTGGCAGAAACACCAATCACTTTAACTAATCTAATTA 5160  
QY 5161 CTGAAGAGACTACTCATGTTGTTATGAAAAACAGATGCTGAGTTGTGTGAAACGACAC 5220

DB 5161 CTGAAGAGACTACTCATGTTGTTATGAAAAACAGATGCTGAGTTGTGTGTAACGGACAC 5220  
QY 5221 TGAATAATTTTCTAGGAATTCGCGGAGGAAAAATGGGTAGTACTATTTCTGGGTGACCC 5280  
DB 5221 TGAATAATTTTCTAGGAATTCGCGGAGGAAAAATGGGTAGTACTATTTCTGGGTGACCC 5280  
QY 5281 AGTCTATTAAGAGAGAAAAATGCTGATGAGCATGATTTTGAAGTCCAGAGGAGATGCG 5340  
DB 5281 AGTCTATTAAGAGAGAAAAATGCTGATGAGCATGATTTTGAAGTCCAGAGGAGATGCG 5340  
QY 5341 TCAATGGAAGAAACCAACCAAGGTCCTCAAGCGAGCAAGAGAAATCCAGGACAGAAAGATCT 5400  
DB 5341 TCAATGGAAGAAACCAACCAAGGTCCTCAAGCGAGCAAGAGAAATCCAGGACAGAAAGATCT 5400  
QY 5401 TCAGGGGGCTAGAAATCTGTTGCTATGGGCCCTTCCACACATGCCACAGATCAACTGG 5460  
DB 5401 TCAGGGGGCTAGAAATCTGTTGCTATGGGCCCTTCCACACATGCCACAGATCAACTGG 5460  
QY 5461 AATGATGTTACAGCTGTGTGTGTCTTCTGTGTGAGGAGCTTTCATCTTCACTTCACTTGG 5520  
DB 5461 AATGATGTTACAGCTGTGTGTGTCTTCTGTGTGAGGAGCTTTCATCTTCACTTCACTTGG 5520  
QY 5521 GCACAGGTGTCACCCCAATTTGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5580  
DB 5521 GCACAGGTGTCACCCCAATTTGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5580  
QY 5581 TCCATGCAATTTGGGCGAGATGT 5640  
DB 5581 TCCATGCAATTTGGGCGAGATGT 5640  
QY 5641 GTGTAGCACTTACAGTCCAGGAGT 5700  
DB 5641 GTGTAGCACTTACAGTCCAGGAGT 5700  
QY 5701 GCCACTACTGA 5711  
DB 5701 GCCACTACTGA 5711

RESULT 11  
AAV46456  
ID AAV46456 standard; cDNA; 5711 BP.  
XX  
AC AAV46456;  
XX  
DT 18-NOV-1998 (first entry)  
XX  
DE Human BRCA1 omil polymorphism #6 cDNA.  
XX  
KW BRCA1; omil; human; breast and ovarian cancer predisposing gene;  
XX  
KW polymorphism; susceptibility; anti-oncogene; tumour suppressor;  
XX  
OS chromosome 17q; ss.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 120..5711  
FT /\*tag= a  
FT /product= "BRCA1 omil protein"  
FT variation 4427  
FT /\*tag= b  
FT /note= "This polymorphic variation can be a T or C  
FT nucleotide"  
XX  
XX US5750400-A.  
XX  
XX PD 12-MAY-1998.  
XX  
XX PD 12-FEB-1997; 97US-00798691.  
XX  
XX PD 12-FEB-1996; 96US-00598591.  
XX

(ONCO-) ONCORMED INC.

Olson SJ, Murphy PD, Zeng B, Alvares CP, Schelter DB, Allen AC;  
Critz BS;

WPI; 1998-296774/26.

BRCA1 omi gene coding sequences - useful for distinguishing between  
polymorphisms and mutation(s) in the screening for disposition to breast  
or ovarian cancer.

Claim 2e; Page; 54pp; English.

This sequence encodes a human BRCA1 (breast and ovarian cancer  
predisposing gene) omi gene in which a polymorphic variation occurs at  
nucleotide 4427. This sequence and other polymorphic variations of this  
sequence are useful for the identification of an individual who may or  
may not have an increased susceptibility to breast or ovarian cancer. The  
sequences used identify gene changes which are due to polymorphisms,  
rather than cancer causing mutations. BRCA1 is an anti-oncogene (tumour  
suppressor) which is involved in genetic inheritance of cancers,  
especially breast and ovarian cancer. It is found at human chromosome 17q  
which is known to be linked to cancer susceptibility, especially breast  
cancer. Cells containing a mutation in this gene lose the wild-type  
function of BRCA1 and are more susceptible to cancers. NOTE: This  
sequence does not appear in the specification but has been created from  
the wild type BRCA1 omi gene represented in AA46448

SQ Sequence 5711 BP; 1953 A; 1098 C; 1277 G; 1382 T; 0 U; 1 Other;

Query Match 100.0%; Score 5710.6; DB 2; Length 5711;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 5710; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy	1	AGCTCGCTGAGACTTCTGACCCCGCACAGGCTGTGGGGTTTCTCAGATAACTGGGCC	60
Db	1	AGCTCGCTGAGACTTCTGACCCCGCACAGGCTGTGGGGTTTCTCAGATAACTGGGCC	60
Qy	61	CCTCGCTCAGAGGCCCTTACCCCTCTGCTGGGTAAAGTTCATTGGAACAGAA	120
Db	61	CCTCGCTCAGAGGCCCTTACCCCTCTGCTGGGTAAAGTTCATTGGAACAGAA	120
Qy	121	TGGATTTATCTGCTTGGGTTGAAGAAGTACAAATGTCAATTAATGTCAGAAAA	180
Db	121	TGGATTTATCTGCTTGGGTTGAAGAAGTACAAATGTCAATTAATGTCAGAAAA	180
Qy	181	TCTTAGAGTCCCATCTGCTGAGTTGATCAAGAACTGTCTCCAAAGTGTGACC	240
Db	181	TCTTAGAGTGTCCCATCTGCTGAGTTGATCAAGAACTGTCTCCAAAGTGTGACC	240
Qy	241	ACATATTTTGCATTTTGCATGCTGAAACTTCTCAACCCAGAGAAAGGCCCTTCAAGT	300
Db	241	ACATATTTTGCATTTTGCATGCTGAAACTTCTCAACCCAGAGAAAGGCCCTTCAAGT	300
Qy	301	GTCCCTTATGTAGAAATGATATACCAAAAGGAGCCCTCAAGAAAGTACAGATTAGTC	360
Db	301	GTCCCTTATGTAGAAATGATATACCAAAAGGAGCCCTCAAGAAAGTACAGATTAGTC	360
Qy	361	AACCTTGTGAAGAGCTATTGAAATCAATTTGTGCTTTTTCAGCTTGACAGGTTTGGAGT	420
Db	361	AACCTTGTGAAGAGCTATTGAAATCAATTTGTGCTTTTTCAGCTTGACAGGTTTGGAGT	420
Qy	421	ATGCAAAACAGCTATAATTTTGCAAAAGGAAATTAATCTCTCTGAACTCTAAAGATG	480
Db	421	ATGCAAAACAGCTATAATTTTGCAAAAGGAAATTAATCTCTCTGAACTCTAAAGATG	480
Qy	481	AGTTTCTATCTCCAAAGTATGGCTACAGAAACCGTGCCTGCAAGCTTCTACAGATG	540
Db	481	AGTTTCTATCTCCAAAGTATGGCTACAGAAACCGTGCCTGCAAGCTTCTACAGATG	540
Qy	541	AACCCGAAATCTCTCTCCAGGAAACCAAGTCTCAGTGTCCAACTCTCTAACTTTGAA	600
Db	541	AACCCGAAATCTCTCTCCAGGAAACCAAGTCTCAGTGTCCAACTCTCTAACTTTGAA	600

Qy	601	CTGTGAACTCTGAGGACAAAGCAGCGGATACAACTCAAAAGAGCTGTGTCTACATTG	660
Db	601	CTGTGAACTCTGAGGACAAAGCAGCGGATACAACTCAAAAGAGCTGTGTCTACATTG	660
Qy	661	AATTGGGATCTGATTTCTTCTGAAGATACCTTAAAGGCAACTTATGTCAGTGTGGAG	720
Db	661	AATTGGGATCTGATTTCTTCTGAAGATACCTTAAAGGCAACTTATGTCAGTGTGGAG	720
Qy	721	ATCAGGAATTTGTTACAAATCACCCCTCAAGAACCCAGGATGAATTCAGTTTGGATCTG	780
Db	721	ATCAGGAATTTGTTACAAATCACCCCTCAAGAACCCAGGATGAATTCAGTTTGGATCTG	780
Qy	781	CAAAAAAGGCTGCTTGTGAATTTCTGAGACGGATGTAAACAAATCTGAAACATCATCAAC	840
Db	781	CAAAAAAGGCTGCTTGTGAATTTCTGAGACGGATGTAAACAAATCTGAAACATCATCAAC	840
Qy	841	CCAGTAATATGTTGAAACACCACTGAGAGAGCGTGCAGCTGAGAGGCATCCAGAAAGT	900
Db	841	CCAGTAATATGTTGAAACACCACTGAGAGAGCGTGCAGCTGAGAGGCATCCAGAAAGT	900
Qy	901	ATCAGGAGTCTTCTGTTTCAAACTTGCATGTCAGGACCATGTGCACAAATCTCATGCCA	960
Db	901	ATCAGGAGTCTTCTGTTTCAAACTTGCATGTCAGGACCATGTGCACAAATCTCATGCCA	960
Qy	961	GCTCATTTACAGCATGAGACAGCAGTTTATTACTACTAAAGACAGAAATGAATGTAGAAA	1020
Db	961	GCTCATTTACAGCATGAGACAGCAGTTTATTACTACTAAAGACAGAAATGAATGTAGAAA	1020
Qy	1021	AGCTGAAATTTCTTAATAAAGCAACAGCCTCGCTTAGCAAGGAGCCACATAACAGAT	1080
Db	1021	AGCTGAAATTTCTTAATAAAGCAACAGCCTCGCTTAGCAAGGAGCCACATAACAGAT	1080
Qy	1081	GGGCTGGAAGTAAAGAAACATGTAAATGATAGCGGACTCCACACAGAAAAAGGTAG	1140
Db	1081	GGGCTGGAAGTAAAGAAACATGTAAATGATAGCGGACTCCACACAGAAAAAGGTAG	1140
Qy	1141	ATCTGATGCTGATCCCTGCTGTGAGAGAAAGATGGAAATAGGAGAACTGCCATGCT	1200
Db	1141	ATCTGATGCTGATCCCTGCTGTGAGAGAAAGATGGAAATAGGAGAACTGCCATGCT	1200
Qy	1201	CAGAGAACTCTAGAGATACCTGAGAGATGTTCTTTGGATACACTAATAGCAGCATTCAGA	1260
Db	1201	CAGAGAACTCTAGAGATACCTGAGAGATGTTCTTTGGATACACTAATAGCAGCATTCAGA	1260
Qy	1261	AACTTAATGAGTGGTTTCCAGAGAGTGAATGTTAGTGTCTGATGATCAGATGATG	1320
Db	1261	AACTTAATGAGTGGTTTCCAGAGAGTGAATGTTAGTGTCTGATGATCAGATGATG	1320
Qy	1321	GGGAGTCTGAATCAAAATGCCAAAGTAGCTGATGTTATGACAGCTTCTAATAGGATAGTG	1380
Db	1321	GGGAGTCTGAATCAAAATGCCAAAGTAGCTGATGTTATGACAGCTTCTAATAGGATAGTG	1380
Qy	1381	AATATTTCTGGTCTTCAGAGAAATAGACTTACTGCGCAGTGTATCTCATGAGGCTTTAA	1440
Db	1381	AATATTTCTGGTCTTCAGAGAAATAGACTTACTGCGCAGTGTATCTCATGAGGCTTTAA	1440
Qy	1441	TATGTAAAAGTGAAGAGTTCACTCCAAATCAGTAGAGAGTAAATATTGAAGACAAATAT	1500
Db	1441	TATGTAAAAGTGAAGAGTTCACTCCAAATCAGTAGAGAGTAAATATTGAAGACAAATAT	1500
Qy	1501	TTGGGAAACCTTATCGGAGAAAGGCAAGCCTCCCAACTTAAGCCATGTAACTGAAATC	1560
Db	1501	TTGGGAAACCTTATCGGAGAAAGGCAAGCCTCCCAACTTAAGCCATGTAACTGAAATC	1560
Qy	1561	TAATTTATAGGCATTTGTTACTGAGCCACAGATTAACAAGCGTCCCTCCACAAATA	1620
Db	1561	TAATTTATAGGCATTTGTTACTGAGCCACAGATTAACAAGCGTCCCTCCACAAATA	1620
Qy	1621	AATTAAGGTAAGGAGACCTACATCAGGCTTCTCATCTCCTGAGGATTTTATCAAGAAAG	1680
Db	1621	AATTAAGGTAAGGAGACCTACATCAGGCTTCTCATCTCCTGAGGATTTTATCAAGAAAG	1680



[illegible]

D	b	2761	AATGTGCAACAACTTCTTGCCCAACTCTGGGTCCTTTAAGAGAAAACAAGTCCAAAAAGTCACATT	2820
Q	y	2821	TTGAATGTGAACAAAGGAGAAATCNAGCAAAGAATGAGTCTAATATTCAGACCCTGTAC	2880
D	b	2821	TTGAATGTGAACAAAGGAGAAATCNAGCAAAGAATGAGTCTAATATTCAGACCCTGTAC	2880
Q	y	2881	AGACAGTTAATATCATCTGCAGCGCTTCTCTGTGGTTCGAGAAAGATAAGCAGGTA	2940
D	b	2881	AGACAGTTAATATCATCTGCAGCGCTTCTCTGTGGTTCGAGAAAGATAAGCAGGTA	2940
Q	y	2941	ATGCCAAATGTAGTATCAAAAGGAGGCTCTAGGTTTTGTCTATCATCTCAGTTTCAGAGCCA	3000
D	b	2941	ATGCCAAATGTAGTATCAAAAGGAGGCTCTAGGTTTTGTCTATCATCTCAGTTTCAGAGCCA	3000
Q	y	3001	ACGAAACTGGACTCATTTCTCCAAATAAACATGGACTTTTACAAAACCCATATCGTATAC	3060
D	b	3001	ACGAAACTGGACTCATTTCTCCAAATAAACATGGACTTTTACAAAACCCATATCGTATAC	3060
Q	y	3061	CACCACATTTTCCCACATCAGTCAATTTGTTTAAACTAAATGTATGATGAAATCTGCTAGAGG	3120
D	b	3061	CACCACATTTTCCCACATCAGTCAATTTGTTTAAACTAAATGTATGATGAAATCTGCTAGAGG	3120
Q	y	3121	AAAACTTTGAGGAACTTCAATGCTCACCTGMAAGAGAAATGGAAATFGAGAACTTCCAA	3180
D	b	3121	AAAACTTTGAGGAACTTCAATGCTCACCTGMAAGAGAAATGGAAATFGAGAACTTCCAA	3180
Q	y	3181	GTCAGTGGAGCAAAATTAGCCGTAATAACATTAGAGAAAAATGTTTTAAAGGAGCCAGCT	3240
D	b	3181	GTCAGTGGAGCAAAATTAGCCGTAATAACATTAGAGAAAAATGTTTTAAAGGAGCCAGCT	3240
Q	y	3241	CAAGCAATATTAATGAAGTAGGTTCCAGTACTAATGAAGTGGGCTCCAGTATTATGAAA	3300
D	b	3241	CAAGCAATATTAATGAAGTAGGTTCCAGTACTAATGAAGTGGGCTCCAGTATTATGAAA	3300
Q	y	3301	TAGTTCCAGTGATGAAACATTTCAAGCAGAACTAGGTAGAAACAGAGGGCCAAATTTGA	3360
D	b	3301	TAGTTCCAGTGATGAAACATTTCAAGCAGAACTAGGTAGAAACAGAGGGCCAAATTTGA	3360
Q	y	3361	ATGCTATGCTTAGATTAGGGTTTTCCAACTGAGGTCTATAAACAAAGTCTTCTCTGAA	3420
D	b	3361	ATGCTATGCTTAGATTAGGGTTTTCCAACTGAGGTCTATAAACAAAGTCTTCTCTGAA	3420
Q	y	3421	GTAATTGTAAAGCATCTGAAATAAAAAAGCAAGATATCAAGAACTAGTTCAGACTGTTA	3480
D	b	3421	GTAATTGTAAAGCATCTGAAATAAAAAAGCAAGATATCAAGAACTAGTTCAGACTGTTA	3480
Q	y	3481	ATACAGATTTCTCTCCATATCTGATTTTCAGATAA CTTAGAACAGCCTATGGAGAGTGC	3540
D	b	3481	ATACAGATTTCTCTCCATATCTGATTTTCAGATAA CTTAGAACAGCCTATGGAGAGTGC	3540
Q	y	3541	ATGCATCTCAGGTTTTGTTCTGAGACACCTGATGACCTGTTAGATGATGTGAAATAAAGG	3600
D	b	3541	ATGCATCTCAGGTTTTGTTCTGAGACACCTGATGACCTGTTAGATGATGTGAAATAAAGG	3600
Q	y	3601	AAGNACTAGTTTTGCTGAAATGACATTTAAGGAAAGTTCTGCTGTTTTTAGCAAAAGCG	3660
D	b	3601	AAGNACTAGTTTTGCTGAAATGACATTTAAGGAAAGTTCTGCTGTTTTTAGCAAAAGCG	3660
Q	y	3661	TCCAGAGAGAGAGCTTAGCAGAGTCCTAGCCCTTTTACCACATACACATTTGGGCTCAGG	3720
D	b	3661	TCCAGAGAGAGAGCTTAGCAGAGTCCTAGCCCTTTTACCACATACACATTTGGGCTCAGG	3720
Q	y	3721	GTTACCGAGAGGGGCCAAGAAATTAGAGTCTCTCAGAGAGAACTTATCTAGTGAGGATG	3780
D	b	3721	GTTACCGAGAGGGGCCAAGAAATTAGAGTCTCTCAGAGAGAACTTATCTAGTGAGGATG	3780
Q	y	3781	AAGAGCTTCCCTGCTTCCAACTGTTATTTGTTAAAGTAAACATATACCTCTCCAGT	3840
D	b	3781	AAGAGCTTCCCTGCTTCCAACTGTTATTTGTTAAAGTAAACATATACCTCTCTCAGT	3840
Q	y	3841	CTACTAGGCATAGCACCGTTGCTGCTACGAGTGTCTGCTTAAGAAACAGAGAGAAATTTAT	3900

Db 3841 CTACTAGGATAGCACCGTTGCTACCGAGTGTCTGTCTAGAAACACAGAGGAGAAATTAT 3900  
Qy 3901 TATCAATTGAAGATAGCTTTAAATGACTGCAGTAAACAGGTAATATTTGGCAAGGCACTTC 3960  
Db 3901 TATCAATTGAAGATAGCTTTAAATGACTGCAGTAAACAGGTAATATTTGGCAAGGCACTTC 3960  
Qy 3961 AGGAACATCACTTAGTAGGAGAAACAAATATTTCTGTAGCTTTCTTCAAGTGCA 4020  
Db 3961 AGGAACATCACTTAGTAGGAGAAACAAATATTTCTGTAGCTTTCTTCAAGTGCA 4020  
Qy 4021 GTGAATTTGGAGAGCTTGAAGTCAATCAAAACACCCAGGATCTTTCTTGAATTTGGTTC 4080  
Db 4021 GTGAATTTGGAGAGCTTGAAGTCAATCAAAACACCCAGGATCTTTCTTGAATTTGGTTC 4080  
Qy 4081 CCAACAAATAGGAGATCAGTCTGAAGCCAGGAGTTGGTCTGAGTGACAGGAATTTGG 4140  
Db 4081 CCAACAAATAGGAGATCAGTCTGAAGCCAGGAGTTGGTCTGAGTGACAGGAATTTGG 4140  
Qy 4141 TTTTCAGATGATGAGAGAGAGAGAGGCTTTGGAGAAATTAATCAAGAGAGCAAGCA 4200  
Db 4141 TTTTCAGATGATGAGAGAGAGAGAGGCTTTGGAGAAATTAATCAAGAGAGCAAGCA 4200  
Qy 4201 TGGATTCAAATCTAGGTGAAGCAGCATCTGGGTGTGAGAGTGAACCAAGGCTCTCTGAAG 4260  
Db 4201 TGGATTCAAATCTAGGTGAAGCAGCATCTGGGTGTGAGAGTGAACCAAGGCTCTCTGAAG 4260  
Qy 4261 ACTGCTCAGGGCTATTCCTCTCAGAGTGACATTTTAAACACTCAGCAGAGGATACCATG 4320  
Db 4261 ACTGCTCAGGGCTATTCCTCTCAGAGTGACATTTTAAACACTCAGCAGAGGATACCATG 4320  
Qy 4321 AACATAACCTGATTAAGCTCCAGCAGAGAGATGGCTGAAGTGAAGTGTGTAGAACAGC 4380  
Db 4321 AACATAACCTGATTAAGCTCCAGCAGAGAGATGGCTGAAGTGAAGTGTGTAGAACAGC 4380  
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Db 4381 ATGGAGCCAGCCTTTCTAACAGTACCTTTCCATATAAGTGAATCTTTCTGCCCTTGAGG 4440  
Qy 4441 ACCTGCGAATCCAGAACAGCAGATCAGAGAGAGAGTATTAATCTTACAGAAAGTA 4500  
Db 4441 ACCTGCGAATCCAGAACAGCAGATCAGAGAGAGAGTATTAATCTTACAGAAAGTA 4500  
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Db 4501 GTGAATACCTTATAAGCCAGAAATCCAGAGGCTTTCTGTGTGAACAAGTTTGAGGTCTG 4560  
Qy 4561 CAGATAGTTTACAGTAAATAAAGAACAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 4620  
Db 4561 CAGATAGTTTACAGTAAATAAAGAACAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 4620  
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Db 4621 GCCCATCAATTAGATGATAGTGGTACATGACAGTGTCTCTGGAGTCTTCAGAAATAGAA 4680  
Qy 4681 ACTACCAATCTCAAGAGAGCTCAATTAAGTGTGTGATGAGAGGAGCAACAGCTGGAAG 4740  
Db 4681 ACTACCAATCTCAAGAGAGCTCAATTAAGTGTGTGATGAGAGGAGCAACAGCTGGAAG 4740  
Qy 4741 AGTCTGGGCCACACGATTTGAGGAGAACATCTTACTTCCAGAGCAGAGATCTAGAGGAA 4800  
Db 4741 AGTCTGGGCCACACGATTTGAGGAGAACATCTTACTTCCAGAGCAGAGATCTAGAGGAA 4800  
Qy 4801 CCCCTTACCTGGATCTGGAATCAGCTCTTCTGTGATGACCCCTGATCTGTATCTCTCTG 4860  
Db 4801 CCCCTTACCTGGATCTGGAATCAGCTCTTCTGTGATGACCCCTGATCTGTATCTCTCTG 4860  
Qy 4861 AAGACAGAGCCAGAGTCAAGTGTGTGGACATACATCTTCAACCTTCAACCTTCAACCTTCA 4920  
Db 4861 AAGACAGAGCCAGAGTCAAGTGTGTGGACATACATCTTCAACCTTCAACCTTCAACCTTCA 4920  
Qy 4921 AAGTTCCCAATTTGAAGTTGCAGATCTGCCCCAGGCTCCAGCTGCTGCTACTACTG 4980  
Db 4921 AAGTTCCCAATTTGAAGTTGCAGATCTGCCCCAGGCTCCAGCTGCTGCTACTACTG 4980

Qy 4981 AFACTGCTGGTATATGCAATCGAAGAAAGTGTGAGCAGGAGAGAACCCAGATTGACAG 5040  
Db 4981 ATACTGCTGGGTATTAATGCAATGGAAGAAAGTGTGAGCAGGAGAGAACCCAGATTGACAG 5040  
Qy 5041 CTTCAACAGAAAGGGTCAACAAAGAAAGTGTCCATGGTGGTGTCTGGCTCAGCCAGAG 5100  
Db 5041 CTTCAACAGAAAGGGTCAACAAAGAAAGTGTCCATGGTGGTGTCTGGCTCAGCCAGAG 5100  
Qy 5101 AATTTATGCTGCTGTACAGTTTGCAGAAACACACCAATCATCTTTAACTAATCTAATTA 5160  
Db 5101 AATTTATGCTGCTGTACAGTTTGCAGAAACACACCAATCATCTTTAACTAATCTAATTA 5160  
Qy 5161 CTGAGAGAGACTACTCATGTTGTTATGAAAACAGATGCTGAGTTTGTGTGAAAGGAGCAC 5220  
Db 5161 CTGAGAGAGACTACTCATGTTGTTATGAAAACAGATGCTGAGTTTGTGTGAAAGGAGCAC 5220  
Qy 5221 TGAATATTTTCTAGGAATTTGGGAGGAGAAATTTGGGTAGTTAGCTATTTCTGGTGAACCC 5280  
Db 5221 TGAATATTTTCTAGGAATTTGGGAGGAGAAATTTGGGTAGTTAGCTATTTCTGGTGAACCC 5280  
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Db 5281 AGTCTATTAAAGAAAGAAATTCGCTGAATGAGCATGATTTGAAAGTCAGAGGAGATGTGG 5340  
Qy 5341 TCAATCGAAAGAAACCAACCAAGGTCCAAAGCGAGCAAGAGAAATCCAGGAACAGAAATCT 5400  
Db 5341 TCAATCGAAAGAAACCAACCAAGGTCCAAAGCGAGCAAGAGAAATCCAGGAACAGAAATCT 5400  
Qy 5401 TCAGGGGGCTAGAAATCTGCTATGTCATGGGCCCTTCCACCAATGCCCAACAGATCAACTGG 5460  
Db 5401 TCAGGGGGCTAGAAATCTGCTATGTCATGGGCCCTTCCACCAATGCCCAACAGATCAACTGG 5460  
Qy 5461 AATGGATGCTTACAGCTGTGTGGTCTTCTGTGTGAGGAGCTTTTCATTCATTCACCTTTG 5520  
Db 5461 AATGGATGCTTACAGCTGTGTGGTCTTCTGTGTGAGGAGCTTTTCATTCATTCACCTTTG 5520  
Qy 5521 GCACAGGTGTCACCCCAATTTGGTGTGTGTCAGCCAGATGCTGGAAGAGGACATGGCT 5580  
Db 5521 GCACAGGTGTCACCCCAATTTGGTGTGTGTCAGCCAGATGCTGGAAGAGGACATGGCT 5580  
Qy 5581 TCCATCAATTTGGGCAAGATGTGTAGGCCACCTGTGTGTGACCCGAGAGTGGGTGTTGGACA 5640  
Db 5581 TCCATCAATTTGGGCAAGATGTGTAGGCCACCTGTGTGTGACCCGAGAGTGGGTGTTGGACA 5640  
Qy 5641 GTGTAGCACTCTTACAGTGCAGGAGCTGGAACCTTACTGTATACCCAGATCCCCCACA 5700  
Db 5641 GTGTAGCACTCTTACAGTGCAGGAGCTGGAACCTTACTGTATACCCAGATCCCCCACA 5700  
Qy 5701 GCCACTACTGA 5711  
Db 5701 GCCACTACTGA 5711

## RESULT 12

AAV46471

ID AAV46471 standard; cDNA; 5711 BP.

XX AAV46471;

AC AAV46471;

XX 18-NOV-1998 (first entry)

XX Human BRCA1 omi3 polymorphism #7 cDNA.

XX BRCA1; omi3; human; breast and ovarian cancer predisposing gene;

XX polymorphism; susceptibility; anti-oncogene; tumour suppressor;

XX chromosome 17q; ss.

XX Homo sapiens.

XX Key

XX Location/Qualifiers

XX 120...5711

XX /\*tag= a

```

FT variation /product= "BRCA1 omi3 protein"
FT 4956 /tag= b
FT /note= "This polymorphic variation can be an A or G
FT nucleotide"
XX
XX US5750400-A.
XX
XX PD 12-MAY-1998.
XX
XX PF 12-FEB-1997; 97US-00798691.
XX
XX PR 12-FEB-1996; 96US-00598591.
XX
XX PA (ONCO-) ONCORMED INC.
XX
XX P1 Olson SJ, Murphy PD, Zeng B, Alvares CP, Schelter DB, Allen AC,
XX P2 Critz BS;
XX
XX PS WPI; 1998-296774/26.
XX
XX CC This sequence encodes a human BRCA1 (breast and ovarian cancer
XX predisposing gene) omi3 gene in which a polymorphic variation occurs at
XX nucleotide 4956. This sequence and other polymorphic variations of this
XX sequence are useful for the identification of an individual who may or
XX may not have an increased susceptibility to breast or ovarian cancer. The
XX sequences used identify gene changes which are due to polymorphisms,
XX rather than cancer causing mutations. BRCA1 is an anti-oncogene (tumour
XX suppressor) which is involved in genetic inheritance of cancers,
XX especially breast and ovarian cancer. It is found at human chromosome 17q
XX which is known to be linked to cancer susceptibility, especially breast
XX cancer. Cells containing a mutation in this gene lose the wild-type
XX function of BRCA1 and are more susceptible to cancers. NOTE: This
XX sequence does not appear in the specification but has been created from
XX the wild type BRCA1 omi3 gene represented in AAV46450
XX
XX SQ Sequence 5711 BP; 1953 A; 1098 C; 1276 G; 1383 T; 0 U; 1 Other;

Query Match 100.0%; Score 5710.6; DB 2; Length 5711;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5710; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGGCTGAGACTTCCTGGACCCCGCACAGGCTGTGGGGTTCTCAGATACTGGCCC 60
DB |||||||
QY 1 AGCTGGCTGAGACTTCCTGGACCCCGCACAGGCTGTGGGGTTCTCAGATACTGGCCC 60
DB |||||||
QY 61 CTGCGCTCAGAGGCGCTTCAACCCTCTGCTGGGTAAAGTTCAATTGGAAACAGAAAGAAA 120
DB |||||||
QY 61 CTGCGCTCAGAGGCGCTTCAACCCTCTGCTGGGTAAAGTTCAATTGGAAACAGAAAGAAA 120
DB |||||||
QY 121 TGGATTTATCTGCTTCGGGTGAAGAGTACAAATGTCATTAATGCTATGCGAGAAA 180
DB |||||||
QY 121 TGGATTTATCTGCTTCGGGTGAAGAGTACAAATGTCATTAATGCTATGCGAGAAA 180
DB |||||||
QY 181 TCTTAGAGTGTCCCATCTGCTGAGTTGATCAAGGAACCTGTCTCCACAAAGTGTGACC 240
DB |||||||
QY 181 TCTTAGAGTGTCCCATCTGCTGAGTTGATCAAGGAACCTGTCTCCACAAAGTGTGACC 240
DB |||||||
QY 241 ACATATTTTGCMAATTTTGATGCTGAAACTTCTCAACGACGAGAAAGGCGCTTCACAGT 300
DB |||||||
QY 241 ACATATTTTGCMAATTTTGATGCTGAAACTTCTCAACGACGAGAAAGGCGCTTCACAGT 300
DB |||||||
QY 301 GTCCCTTTATGTAGAGATGATATAACCAAGAGGCGCTTACAAAGAAAGTACGAGATTTAGTC 360
DB |||||||
QY 301 GTCCCTTTATGTAGAGATGATATAACCAAGAGGCGCTTACAAAGAAAGTACGAGATTTAGTC 360
DB |||||||
QY 361 AACTGTGTGAGAGCTATTGMAATCATTTTGTGCTTTTACGCTTGACACAGGTTGGAGT 420
DB |||||||

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DB 361 AACTGTGTGAGAGCTATTGAAATCATTTTGTGCTTTTTCAGCTTGACACAGGTTGGAGT 420
QY 421 ATGCAAAACAGCTATAATTTTGCRAAAAGGAAATTAATCTCTCTGACATCTTAAAGATG 430
DB 421 ATGCAAAACAGCTATAATTTTGCRAAAAGGAAATTAATCTCTCTGACATCTTAAAGATG 480
QY 481 AAGTTTCTATCATCCAAAGTATGGGCTACAGAAACCGTGCCAAAGAGCTTCTACAGAGTG 540
DB 481 AAGTTTCTATCATCCAAAGTATGGGCTACAGAAACCGTGCCAAAGAGCTTCTACAGAGTG 540
QY 541 AACCCGAAATCTCTCTGCGAGAAACAGTCTCAGTGTCCACTCTCTAACCTTGCAA 600
DB 541 AACCCGAAATCTCTCTGCGAGAAACAGTCTCAGTGTCCACTCTCTAACCTTGCAA 600
QY 601 CTGTGAGAACTCTGAGGACAAAGCAGCGGATACAACTCAAGAGACCTCTGTCTACATTG 660
DB 601 CTGTGAGAACTCTGAGGACAAAGCAGCGGATACAACTCAAGAGACCTCTGTCTACATTG 660
QY 661 AATGGGATCTGATTTCTCTGAAGATACCGTTAATAGGCACTTATTCAGTGTGGAG 720
DB 661 AATGGGATCTGATTTCTCTGAAGATACCGTTAATAGGCACTTATTCAGTGTGGAG 720
QY 721 ATCAAGAAATTTTACAAATCAACCCCTCAAGAAACCGGATGAAATCAGTTTGGATCTG 780
DB 721 ATCAAGAAATTTTACAAATCAACCCCTCAAGAAACCGGATGAAATCAGTTTGGATCTG 780
QY 781 CAAAAAGGCTGCTGTGTAATTTTCTGAGACGGATGTAAACAAATATCTGAACATCATCAAC 840
DB 781 CAAAAAGGCTGCTGTGTAATTTTCTGAGACGGATGTAAACAAATATCTGAACATCATCAAC 840
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DB 841 CCAGTAAATATGATTTTGAACACCACTGAGAAAGCTGAGCTGAGAGGCACTCCAGAAAGT 900
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DB 901 ATCAGGATGCTCTGTTTCAAACTGTGATGTGAGGCACTGTGCAAAATATCTCATGCCA 960
QY 961 GCTCATTACAGCATGAGACAGCAGTTTATCTCTCACTAAGACAGAAATGAATGTAGAA 1020
DB 961 GCTCATTACAGCATGAGACAGCAGTTTATCTCTCACTAAGACAGAAATGAATGTAGAA 1020
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DB 1021 AGGCTGAATTTCTGTAATAAAAGCAACAGCTGGCTTAGCAAGGAGCCCAACATPACAGAT 1080
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DB 1081 GGGCTGGAAGTAAAGGAACATGTATGATAGGGGACTCCAGCACAGAAAGAGGTAG 1140
QY 1141 ATCTGAATGCTGATCCCTGCTGTGAGAGAAAGAAATGGAATAGCAGAAACTGCCATGCT 1200
DB 1141 ATCTGAATGCTGATCCCTGCTGTGAGAGAAAGAAATGGAATAGCAGAAACTGCCATGCT 1200
QY 1201 CAGAGAACTCTAGAGATCTGAAGATGTTCTTTGGATTAACACTAAATAGCAGCATTCAGA 1260
DB 1201 CAGAGAACTCTAGAGATCTGAAGATGTTCTTTGGATTAACACTAAATAGCAGCATTCAGA 1260
QY 1261 AAGTTAATCAGTGTGTTTCCAGAGTGTGAATCTGTAGTGTCTGATGACTCAGCATGAG 1320
DB 1261 AAGTTAATCAGTGTGTTTCCAGAGTGTGAATCTGTAGTGTCTGATGACTCAGCATGAG 1320
QY 1321 GGGAGTCTGAATCAAAATGCAAGTAGCTGATGTATTTGACCTTTCTAAATAGGTTAGATG 1380
DB 1321 GGGAGTCTGAATCAAAATGCAAGTAGCTGATGTATTTGACCTTTCTAAATAGGTTAGATG 1380
QY 1381 AATATTCTGGTCTTTCAGAGAAATAGACTTACTGCGCAGATGATCTCTCATAGGCTTTAA 1440
DB 1381 AATATTCTGGTCTTTCAGAGAAATAGACTTACTGCGCAGATGATCTCTCATAGGCTTTAA 1440
QY 1441 TATGTAAAGTCAAGAGTTCACTCAATCAGTAGAGATTAATTTGAGACAAATAT 1500
DB |||||||

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QY	3661	TC	CAGAGAGGAGAGCTTACGAGGAGTCTCTAGCCCTTTACCCATACACATTTGGCTCAGG	3720
DB	3661	TC	CAGAGAGGAGAGCTTACGAGGAGTCTCTAGCCCTTTACCCATACACATTTGGCTCAGG	3720
QY	3721	GT	TACCCGAAGGGGCCAAGAAATTAGAGTCTCTCAGAAGAGAACTTATCTAGTGTGAGGATG	3780
DB	3721	GT	TACCCGAAGGGGCCAAGAAATTAGAGTCTCTCAGAAGAGAACTTATCTAGTGTGAGGATG	3780
QY	3781	AAG	AGCTTCCCTTGCCTTCCAAACACTTGTATTTGGTAAAGTAAACAAATATACCTTCTCAGT	3840
DB	3781	AAG	AGCTTCCCTTGCCTTCCAAACACTTGTATTTGGTAAAGTAAACAAATATACCTTCTCAGT	3840
QY	3841	CT	ACTAGGCATAGCACCGTGTCTACCGAGTCTCTGTCTTAGAAACACAGAGGGAGATTAT	3900
DB	3841	CT	ACTAGGCATAGCACCGTGTCTACCGAGTCTCTGTCTTAGAAACACAGAGGGAGATTAT	3900
QY	3901	TAT	CAATTCAAGAATAGCTTAAATGACTGTCAGTAAACCCAGGTAATATTGGCAAGGCATCTC	3960
DB	3901	TAT	CAATTCAAGAATAGCTTAAATGACTGTCAGTAAACCCAGGTAATATTGGCAAGGCATCTC	3960
QY	3961	AGG	ACATCTACCTTAGTGAGGAAACAAAATGTTCTGTCTAGCTTGTCTTCTTCTACAGTGCA	4020
DB	3961	AGG	ACATCTACCTTAGTGAGGAAACAAAATGTTCTGTCTAGCTTGTCTTCTTCTTCTACAGTGCA	4020
QY	4021	GT	GAATTGGAAAGACTGACTGCCAAATACAAAACACCAGGATCTCTTCTTGATTGGTTCCT	4080
DB	4021	GT	GAATTGGAAAGACTGACTGCCAAATACAAAACACCAGGATCTCTTCTTGATTGGTTCCT	4080
QY	4081	CC	AAACAAATGAGGATCAGTCTGAAAGCCAGGAGTTGGTCTGAGTGAACAAGAAATTTGG	4140
DB	4081	CC	AAACAAATGAGGATCAGTCTGAAAGCCAGGAGTTGGTCTGAGTGAACAAGAAATTTGG	4140
QY	4141	TTT	CAGATGATGAAGAAAGAGAAACGGCTTTGGAAGAAATAATCAAGAAAGCAAGA	4200
DB	4141	TTT	CAGATGATGAAGAAAGAGAAACGGCTTTGGAAGAAATAATCAAGAAAGCAAGA	4200
QY	4201	TGG	ATTCAAACTTAGTGAAGCAGCAGTCTGGTGTGAGAGTGAAAACAAGCGTCTCTGAA	4260
DB	4201	TGG	ATTCAAACTTAGTGAAGCAGCAGTCTGGTGTGAGAGTGAAAACAAGCGTCTCTGAA	4260
QY	4261	ACT	GCTCAGGGCTATCTCTCAGAGTCACATTTTACCACTCAGCAGAGGGATACCATGC	4320
DB	4261	ACT	GCTCAGGGCTATCTCTCAGAGTGACATTTTAACTCTCAGCAGAGGGATACCATGC	4320
QY	4321	AAC	ATAACCTGATAAAGCTTCAGAGGAAATGGCTGAACTAGAGCTGTGTTAGAACAGC	4380
DB	4321	AAC	ATAACCTGATAAAGCTTCAGAGGAAATGGCTGAACTAGAGCTGTGTTAGAACAGC	4380
QY	4381	ATG	GGAGCCAGCTTCTTAAACAGCTACCTTCCATCATAGTGTGACTCTCTGCGCTTGAGG	4440
DB	4381	ATG	GGAGCCAGCTTCTTAAACAGCTACCTTCCATCATAGTGTGACTCTCTGCGCTTGAGG	4440
QY	4441	ACT	TGCAAAATCCAGAACAAAGCACATCGAAAAAGCAGTATTAACTTCACAGAAAGTA	4500
DB	4441	ACT	TGCAAAATCCAGAACAAAGCACATCGAAAAAGCAGTATTAACTTCACAGAAAGTA	4500
QY	4501	GT	GAATACCTTATAGCCAGATCCAGAGGCCCTTTCTGCTGACAAAGTTGAGGTGTCTG	4560
DB	4501	GT	GAATACCTTATAGCCAGATCCAGAGGCCCTTTCTGCTGACAAAGTTGAGGTGTCTG	4560
QY	4561	CAG	ATAGTCTTACCAGTAAAAATAAAGAACCCAGAGTGAAAGTCAATCCCTCTCTAAT	4620
DB	4561	CAG	ATAGTCTTACCAGTAAAAATAAAGAACCCAGAGTGAAAGTCAATCCCTCTCTAAT	4620
QY	4621	GCC	CATCATTAGATGATAGTGTGATACATGCAAGTTGTCTGGAGTCTTCCAGAAATAGAA	4680
DB	4621	GCC	CATCATTAGATGATAGTGTGATACATGCAAGTTGTCTGGAGTCTTCCAGAAATAGAA	4680
QY	4681	ACT	ACCCTCTCAAGAGGAGCTCATTAAGTGTGTGATCTGCGAGAGCAACAGCTGGAG	4740
DB	4681	ACT	ACCCTCTCAAGAGGAGCTCATTAAGTGTGTGATCTGCGAGAGCAACAGCTGGAG	4740
QY	4741	AGT	CTGGGCCACACBAATTTGACGGAACATCTTATCTTGCAAGGCAAGATCTTAGAGGAA	4800

Db	4741	AGTCTGGGGCACACGATTTGTCAGGAAACATCTTACTTGGCCAGGCAAGATCTAGAGGGAA	4800
Qy	4801	CCCCTTACCTGGAAATCTGGAAATCAGCGCTCTTCTCTGATGACCCCTGAATCTGATCCCTTCG	4860
Db	4801	CCCCTTACCTGGAAATCTGGAAATCAGCGCTCTTCTCTGATGACCCCTGAATCTGATCCCTTCG	4860
Qy	4861	AAGA CAGAGCCCCAGAGCTCAGCTCGTGTGTGGCAACATACCATCTTCAACCTCTGCATTGA	4920
Db	4861	AAGA CAGAGCCCCAGAGCTCAGCTCGTGTGTGGCAACATACCATCTTCAACCTCTGCATTGA	4920
Qy	4921	AAGTTCCCCCAATTGAAAGTTGCAGATCTGCCCCAGAGTCCAGCTGCTGCTCATCTACTCTG	4980
Db	4921	AAGTTCCCCCAATTGAAAGTTGCAGATCTGCCCCAGAGTCCAGCTGCTGCTCATCTACTCTG	4980
Qy	4981	ATACTGCTGGGTATAATGCAATGGAAGAAAGTGTGACAGGGAGAACCCAGAATTGCACAG	5040
Db	4981	ATACTGCTGGGTATAATGCAATGGAAGAAAGTGTGACAGGGAGAACCCAGAATTGCACAG	5040
Qy	5041	CTTTCACAGAAAGGGTCAACAAAAGAAATGCCATGTGTGTGTGCTGCTGACCCCGAAG	5100
Db	5041	CTTTCACAGAAAGGGTCAACAAAAGAAATGCCATGTGTGTGTGCTGCTGACCCCGAAG	5100
Qy	5101	AAATTATGCTCGTGTACAAAGTTGGCCAGAAAAACACACATCACTTTAACTAAATCTAAATTA	5160
Db	5101	AAATTATGCTCGTGTACAAAGTTGGCCAGAAAAACACACATCACTTTAACTAAATCTAAATTA	5160
Qy	5161	CTGAAGAGACTACTCATGTGTTATGAAAACAGATGCTGAGTTGTGTGTGAACGGACAC	5220
Db	5161	CTGAAGAGACTACTCATGTGTTATGAAAACAGATGCTGAGTTGTGTGTGAACGGACAC	5220
Qy	5221	TGAAATATTTTCTAGGAATTCGGGGAGGAAAAATGGGTAGTTAGCTATTTCTCGGTGACCC	5280
Db	5221	TGAAATATTTTCTAGGAATTCGGGGAGGAAAAATGGGTAGTTAGCTATTTCTCGGTGACCC	5280
Qy	5281	AGTCTATTAAAGAAAGAAAAATGCTGAAATGAGCATGATTTTGAAGTCAGAGGAGATGTGG	5340
Db	5281	AGTCTATTAAAGAAAGAAAAATGCTGAAATGAGCATGATTTTGAAGTCAGAGGAGATGTGG	5340
Qy	5341	TCAATGGAAGAACACACCAAGGTCCAAAGCGAGCAGAGAAATCCACAGACAGAAAGATCT	5400
Db	5341	TCAATGGAAGAACACCAAGGTCCAAAGCGAGCAGAGAAATCCACAGACAGAAAGATCT	5400
Qy	5401	TCAGGGGGCTAGAAAAATCTGTGCTATGGGCCCTTCAACCAATGCCCCACAGATCAACTGG	5460
Db	5401	TCAGGGGGCTAGAAAAATCTGTGCTATGGGCCCTTCAACCAATGCCCCACAGATCAACTGG	5460
Qy	5461	AATGGAATGGTACAGCTGTGTGTGTGCTCTGTGGTGAAGAGGCTTTTCATCATCCCTTG	5520
Db	5461	AATGGAATGGTACAGCTGTGTGTGTGCTCTGTGGTGAAGAGGCTTTTCATCATCCCTTG	5520
Qy	5521	GCACAGGTGCCACCAAATGTGTGTTGTGCAGCCAGATGCCCTGGACAGAGACCAATGGCT	5580
Db	5521	GCACAGGTGCCACCAAATGTGTGTTGTGCAGCCAGATGCCCTGGACAGAGACCAATGGCT	5580
Qy	5581	TCAATGCAATGGGCGAGATGTGTGAGGCACTGTGGTGAACCGAGAGTGGGTGTGGACA	5640
Db	5581	TCAATGCAATGGGCGAGATGTGTGAGGCACTGTGGTGAACCGAGAGTGGGTGTGGACA	5640
Qy	5641	GTGTAGCACTCTACAGTCCAGGAGCTGGACACCTCTCTGATACCCCGAGATCCCCACA	5700
Db	5641	GTGTAGCACTCTACAGTCCAGGAGCTGGACACCTCTCTGATACCCCGAGATCCCCACA	5700
Qy	5701	GCCACTACTGA	5711
Db	5701	GCCACTACTGA	5711

RESULT 13  
AAT87085  
ID AAT87085 standard; cDNA; 5711 bp.  
XX  
AC AAT87085;

XX 06-JAN-1998 (first entry)  
 XX Human BRCA1 gene consensus.  
 XX BRCA1 gene; BRCA1(oni); breast cancer; ovary cancer; polymorphism;  
 KW genetic testing; diagnosis; gene therapy; ss.  
 XX Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 120..5711  
 FT variation /\*tag= a  
 FT 2201  
 FT variation /\*tag= b  
 FT position 2201  
 FT 2430  
 FT variation /\*tag= c  
 FT /note= "35-45% TTG (Leu) and 55-65% CTG (Leu)  
 FT polymorphism at position 2430"  
 FT 2731  
 FT variation /\*tag= d  
 FT /note= "25-35% CCG (Pro) and 65-75% CTG (Leu)  
 FT polymorphism at position 2731"  
 FT 3232  
 FT variation /\*tag= e  
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 FT polymorphism at position 3232"  
 FT 3667  
 FT variation /\*tag= f  
 FT /note= "35-45% AAA (Iys) and 55-65% AGA (Arg)  
 FT polymorphism at position 3667"  
 FT 4427  
 FT variation /\*tag= g  
 FT /note= "45-55% TCT (Ser) and 45-55% TCC (Ser)  
 FT polymorphism at position 4427"  
 FT 4936  
 FT variation /\*tag= h  
 FT /note= "35-45% AGT (Ser) and 55-65% GGT (Gly)  
 FT polymorphism at position 4936"  
 XX US5654155-A.  
 XX  
 XX 05-AUG-1997.  
 XX  
 XX 12-FEB-1996; 96US-00598591.  
 XX  
 XX 12-FEB-1996; 96US-00598591.  
 XX  
 XX (ONCO-) ONCORMED INC.  
 XX  
 XX Olson SJ, Allen AC, Zeng B, Schelter DB, Alvares CP, Murphy PD;  
 PI Critz BS;  
 XX  
 XX WPI; 1997-401843/37.  
 XX P-PSDB; AAW26522.  
 XX  
 XX Human BRCA1 gene coding sequence with common normal polymorphisms - for  
 PT assessing susceptibility to breast or ovarian cancer.  
 XX  
 XX Claim 1; Col 19-24; 35pp; English.  
 XX  
 XX This nucleotide sequence comprises a consensus DNA sequence, designated  
 CC BRCA1(oni), for the normal human BRCA1 gene. It was found by end-to-end  
 CC sequencing of the BRCA1 gene from 5 individuals randomly drawn from the  
 CC population and found to have no family history of breast or ovarian  
 CC cancer. The BRCA1(oni) gene and the seven polymorphic sites (which are  
 CC not associated with breast or ovarian cancer) will provide greater  
 CC accuracy and reliability for genetic testing. A claimed method for  
 CC detecting an increased genetic susceptibility to breast and ovarian  
 CC cancer resulting from the presence of a mutation in the BRCA1 coding  
 CC sequence involves amplifying and sequencing the BRCA1 coding sequence

CC from an individual and comparing the sequence with BRCA1(oni). The  
 CC consensus normal BRCA1 sequence can also be used in gene therapy, to make  
 CC diagnostic probes and to express normal BRCA1 polypeptide (see AAW26522)  
 XX  
 XX Sequence 5711 BP; 1953 A; 1099 C; 1277 G; 1382 T; 0 U; 0 Other;  
 SQ  
 Query Match 100.0%; Score 5709.4; DB 2; Length 5711;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 5710; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 AGCTCGCTGAGACTTCTGAGACCCGACACAGGCTGTGGGGTTTCTCAGATAACTGGGCC 60  
 DB 1 AGCTCGCTGAGACTTCTGAGACCCGACACAGGCTGTGGGGTTTCTCAGATAACTGGGCC 60  
 QY 61 CTTGGCGCTCAGGAGGCTTCCACCTCTGCTCTGGTAAAGTTCAATTCGGAACAGAAAGAA 120  
 DB 61 CTTGGCGCTCAGGAGGCTTCCACCTCTGCTCTGGTAAAGTTCAATTCGGAACAGAAAGAA 120  
 QY 121 TGGATTTATCTGCTCTTTCGGTTGAAGAAGTCAAAATGTCAATTAATGCTATGCAGAAA 180  
 DB 121 TGGATTTATCTGCTCTTTCGGTTGAAGAAGTCAAAATGTCAATTAATGCTATGCAGAAA 180  
 QY 181 TCTTAGAGTCTCCATCTGCTGAGGTTGATCAAGAACCTGTCTCCACAAAGTGTGACC 240  
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 DB 241 ACATATTTTGCAAAATTTTGCATGCTCAAACTTCTCAACAGAGAGAGAGGCCCTTCACAGT 300  
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 DB 301 GTCCTTTATGTAGAAATGATATAACCAAAAGGAGCCTACAGAAAGTACGAGATTTAGTC 360  
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 DB 361 AACTCTGTGAGAGCTATTGAAATCAATTTGCTTTTTCAGCTTGCATGACAGGTTTGGAGT 420  
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 DB 421 ATGCAACAGCTATATTTTTCAGAAAGGAGAAATAAATCTCTCTGAAACATCTAAAAAGATG 480  
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 DB 481 AAGTTTCTATCTCAAAAGTATGGGCTACAGAAACCGTGCCAAAAGACTTCTACAGAGTG 540  
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 DB 661 AATTGGGATCTGATTTCTTCTGAGGATACCGTTTAAAGGCACTTATTCAGTGTGGAG 720  
 QY 721 ATCAAGAAATTTTACAAATCAACCTCAAGGAAACAGGAGTGAATCAATTCAGTTTCTG 780  
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 DB 781 CAAAAGAGGCTGCTGTGTAATTTTCTGAGAGGATGTAACAAATCTGAACTATCAATCAAC 840  
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 DB 841 CCAAGTAATGATTTTGAACCACTCTGAGAGGCTGAGAGGATCCAGAAAAGT 900  
 QY 901 ATCAGGAGTGTCTGTTTCAAACTGATGTGGAGCCATGTGGCAAAATCTCATGCCA 960  
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961 GCTCAATTAAGAGATGAGACAGCAGCTTTTATTACTCACTAAAGACAGAGATGAATGTAGAAA 1020  
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1081 GGGCTGGAAGTAAAGAAACATGTATGATAGCGGAGCTCCAGCAACAGAAAAAGGTAG 1140  
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RESULT 14  
 ID AAV46448 standard; cDNA; 5711 BP.

AC AAV46448;

DT 18-NOV-1998 (first entry)

XX Human BRCA1 omil cDNA.

XX BRCA1; omil; human; breast and ovarian cancer predisposing gene;  
 XX polymorphism; susceptibility; anti-oncogene; tumour suppressor;  
 XX chromosome 17q; ss.

XX Homo sapiens.

Key Location/Qualifiers  
 CDS 120..5711  
 /\*tag= a  
 /product= "BRCA1 omil protein"

XX US5750400-A.

XX 12-MAY-1998.

XX 12-FEB-1997; 97US-00798591.

XX 12-FEB-1996; 96US-00598591.

XX (ONCO-) ONCORMED INC.

XX Olsson SJ, Murphy, PD, Zeng B, Alvares CP, Schelter DB, Allen AC;  
 XX Critz BS;

XX WPI; 1998-296774/26.

XX P-PSDB; AAW76098.

XX BRCA1 omi gene coding sequences - useful for distinguishing between  
 XX polymorphisms and mutation(s) in the screening for disposition to breast  
 XX or ovarian cancer.

XX Claim 2d; Col 27-32; 54pp; English.

XX

CC This sequence encodes the human BRCA1 (breast and ovarian cancer  
 CC predisposing gene) omil gene. This sequence and polymorphic variations of  
 CC this sequence are useful for the identification of an individual who may  
 CC or may not have an increased susceptibility to breast or ovarian cancer.  
 CC The sequences used identify gene changes which are due to polymorphisms,  
 CC rather than cancer causing mutations. BRCA1 is an anti-oncogene (tumour  
 CC suppressor) which is involved in genetic inheritance of cancers,  
 CC especially breast and ovarian cancer. It is found at human chromosome 17q  
 CC which is known to be linked to cancer susceptibility, especially breast  
 CC cancer. Cells containing a mutation in this gene lose the wild-type  
 CC function of BRCA1 and are more susceptible to cancers  
 XX  
 SQ Sequence 5711 BP; 1953 A; 1099 C; 1277 G; 1382 T; 0 U; 0 Other;

Query Match 100.0%; Score 5709.4; DB 2; Length 5711;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 5710; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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 QY 601 CTGTGAGAACTCTGAGGACAAAGAGGAGGATACAACTCTCAAGAGAGCTGTCTACATTTG 660  
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 QY 661 AATGGGATCTGATTTCTTGAAGATACCGTTTAAATGAAGCAACTTATTTCAGTGTGGAG 720  
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 QY 721 ATCAGAGATGTTTACAAATCACCCTCAAGAAACAGGAGTGAATTCAGTTTGGATCTG 780  
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DB 1021 AGGCTGAATTCGTAAATAAAGCAACAGCCTGCTTAGCAAGGAGCCCAACATACACAT 1080  
QY 1081 GGGCTGGAAGTAAGCAACATGTAATGATAGCGGAGCTCCAGCAGCAGAAAAAAGGTAG 1140  
DB 1081 GGGCTGGAAGTAAGCAACATGTAATGATAGCGGAGCTCCAGCAGCAGAAAAAAGGTAG 1140  
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Qy 5161 CTGAAGAGACTACTCATGTTGTTATGAAACAGATGCTGAGTTGTTGTTGTTGTTGTTGTTG 5220  
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QY 1141 ATCTGAATCTGATCCCTGTGTGAGAGAAAGAAATGAATAAGCAGAAACCTGCCATGCT 1200  
DB 1141 ATCTGAATCTGATCCCTGTGTGAGAGAAAGAAATGAATAAGCAGAAACCTGCCATGCT 1200  
QY 1201 CAGAGAACTCTAGAGATCTGAAGTGTCTTGGATAACACTAAATAGCAGCACTTCA 1260  
DB 1201 CAGAGAACTCTAGAGATCTGAAGTGTCTTGGATAACACTAAATAGCAGCACTTCA 1260  
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DB 1261 AAGTTAATGAGTGTTCAGAGAGTGAATGAACTGTGTAGGTCTGATGATCAATGATG 1320  
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DB 1321 GGGAGTCTGAATCAAAATCCAAAGTAGCTGATGATTTGGAGCTTCTAAATGAGGTAGTG 1380  
QY 1381 AATATCTGTTCTTTCAGAGAAATAGACTTTACTGGCCAGTGATCCTCATGAGGCTTTAA 1440  
DB 1381 AATATCTGTTCTTTCAGAGAAATAGACTTTACTGGCCAGTGATCCTCATGAGGCTTTAA 1440  
QY 1441 TATGTAAAGTGAAGAGTCTACTCCAAATCAGTAGAGGTAAATATTGAAAGCAAAATAT 1500  
DB 1441 TATGTAAAGTGAAGAGTCTACTCCAAATCAGTAGAGGTAAATATTGAAAGCAAAATAT 1500  
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QY 1561 TAATATAGGAGCATTTGTTACTAGGACCAAGATTAACAAGAGGCTCCCTCAAAATA 1620  
DB 1561 TAATATAGGAGCATTTGTTACTAGGACCAAGATTAACAAGAGGCTCCCTCAAAATA 1620  
QY 1621 AATTAAAGCTGAAAGGAGACTACATCAGGCTTCTCACTCTGAGGATTTTATCAAGAAAG 1680  
DB 1621 AATTAAAGCTGAAAGGAGACTACATCAGGCTTCTCACTCTGAGGATTTTATCAAGAAAG 1680  
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DB 1681 CAGATTGGCAGTTCAAAAGACTCTCTGAAATGAATAATCAGGAACTAAACCAACGGAGC 1740

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QY 1861 AAACGAAAGCTGAACTTATAAGCAGCAGTATAAGCAATATGGAATCTGAAATTAATATCC 1920  
DB 1861 AAACGAAAGCTGAACTTATAAGCAGCAGTATAAGCAATATGGAATCTGAAATTAATATCC 1920  
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DB 1921 ACAATTCAAAAGCACCTTAAAAAAGATAGGCTGAGAGGAAAGTCTTCTACCAAGCATATTC 1980  
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QY 2821 TTGAATGTGAACAAAGGAGAGAAATCAAGGAAAGATGAGTCTAATATATCAAGCCTGTAC 2880



QY 5041 CTTCAACAGAAAGGTCACAAAGAAATGTCATGGTGGTGTCTGGCCTGACCCGAGAAG 5100  
DB |||||||  
QY 5041 CTTCAACAGAAAGGTCACAAAGAAATGTCATGGTGGTGTCTGGCCTGACCCGAGAAG 5100  
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